

SEQUENCE LISTING

<110> Bejanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US2.REG

<140>

<141> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

<150> US 60/293,574

<151> 2001-05-25

<160> 112

<170> JPatent

<210> 1

<211> 2016

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..1434

<220>

<221> CDS

<222> 1435..1836

<220>

<221> 3'UTR

<222> 1837..2016

<220>

<221> polyA_signal

<222> 1965..1970

<220>

<221> polyA_site

<222> 2001..2016

<400> 1

aagggtcttc	tgcatacgata	caccaaggaa	aaggccatcg	aggacataac	caggaagaga	60
gccccatccaca	aaacccggaa	catgcggaca	cctctgatcc	ggacttctag	ccttcggacaa	120
cgttgcacaca	gttttgatga	tcatcttc	cccaaccaag	atgggtggaaa	aagcaaaaac	180
gttgtgtgaaatc	ttggagcaat	ccgcacaaggc	atggaaacgtc	tccaaatttc	gtttaaactgc	240
tgttgagccag	ggacaaatcc	tgtatgcctc	atccctagcag	ctggcttggaa	tctactatgc	300
ggcatttttc	tgatttcattt	tcttcatttt	gtgtgtttt	tctctgtgtat	gtgaatccat	360
cccttacatccat	tgatgtcatgc	ctccatcttt	tgtgtttttt	tcagattgcac	ctgagccata	420
agagggaagcc	cctgtgtgtgg	ccagacgcgc	ctgtttctgt	gaatgtgttc	gttttgttca	480
cccgctcaac	ctgtggcaact	ggccagatgt	gtatggaaagg	caccacgtga	acatcaccaa	540
gaaaaggactt	tcccggggac	gtctccat	tgtggggac	aaggcaaac	agaagctgca	600

gtggaatgca gccaagctct tctaccaatg gggagacaag gaaaaaaaggta gaagaataaa 660
 agggaaattca agaggaccac ttgttgcata atttttagaca gaggtgaaca taaacacaca 720
 taaaagggtt ccataatttc ctctttttttaa aggattact tggtataact gttaacattt 780
 cccgttaataa ttccagctgaa tggtgttacc aatgtgttcc ccaactaagg caattggcgt 840
 cccgttgatgaa gagctgtgcc acggggaaag tgaggtggca gccaaacctgg tgggtctcat 900
 ttacatggaa gagaccaaga ggagacttag aaggaggatg gaggaggaag actttttttaga 960
 tgacatccca cttcaactgaa aatacacacg tcatcttgcata taaaagct gattatgttg 1020
 caagcaactt tcgggctgga aattttctacg aagtgttgc tttccattct tgatggaggg 1080
 caaagtcccc ggcacaataat taactcgagg gagaataatgg ttttccctgaa aaaaacgcata 1140
 gcttaataat cttacagaaag acctgttcc cccacttattt tcaaatggaa tcgtgaaaaa 1200
 cacattttggaa ctagactgaa aacaacttca ctgcctccaa aacagcaaga cagacatccc 1260
 tctaaaatgtt aactgacata atttttatag ctccaaatctt agttcactgc catacata 1320
 gtcataatctt gattgaatag cagcgtagaa atcttgcgaa attacttccc attttctgttt 1380
 tcgttaaaag gtactgtgaa cccctctaaa tgccgttgcc cttttgcctt gaag atg 1437
 Met
 1
 gca gca tgt cag ctt ctg gag att acc acc ttc ctg cga gag acc 1485
 Ala Ala Cys Gln Leu Leu Glu Ile Thr Thr Phe Leu Arg Glu Thr
 5 10 15
 ttt tct tgc ctg ccc aga cct ccc act gag cct ctg qtg gct tca acg 1533
 Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
 20 25 30
 gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581
 Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
 35 40 45
 atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629
 Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys
 50 55 60 65
 gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677
 Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
 70 75 80
 aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac 1725
 Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
 85 90 95
 cag tgt aga gat ggc aaa gtg ggc ttc cag agc ttc ttt tcc cta att 1773
 Gln Cys Arg Asp Gly Lys Val Phe Gln Ser Phe Phe Ser Leu Ile
 100 105 110
 gcg ggc ctc acc att gca tgc aat gac tat ttt gta gta cac atg aag 1821
 Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
 115 120 125
 cag aag gga aag aag taggcagaaaa tgagcagttc gctccccc gataagagtt 1876
 Gln Lys Gly Lys Lys
 130
 gtcccaaaagg gtcgcttaag gaatgtcccc cacagcttcc cccatagaag gatttcatga 1936
 gcagatcagg acacttagca aatgtaaaaa taaaatctaa ctctcatttg acaaggcagag 1996
 aaagaaaaaa aaaaaaaaaat 2016

<210> 2
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Ala Cys Gln Leu Leu Glu Ile Thr Thr Phe Leu Arg Glu
 1 5 10 15
 Thr Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser
 20 25 30
 Thr Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr
 35 40 45
 Met Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr
 50 55 60
 Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu
 65 70 75 80

```

Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu
85 90 95
Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu
100 105 110
Ile Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met
115 120 125
Lys Gln Lys Gly Lys Lys
130

<210> 3
<211> 1081
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..38

<220>
<221> CDS
<222> 39..917

<220>
<221> 3'UTR
<222> 918..1081

<220>
<221> polyA_signal
<222> 1045..1050

<220>
<221> polyA_site
<222> 1066..1081

<400> 3
gtccagcctg ttgctgatgc tgccgtgcgg tactttgtc atg gag ctg gca ctg cgg
Met Glu Leu Ala Leu Arg
-25 -20
Arg Ser Pro Val Pro Arg Trp Leu Leu Leu Leu Pro Leu Leu Gly
-15 -10 -5
104
cgc tct ccc gtc ccg cgg tgg ctg ctg ctg cgg ctg ctg ctg ggc
Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu
1 5 10
152
ctg aac gca gga gct gtc att gac tgg ccc aca gag gag ggc aag gaa
Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu
1 5 10
200
gta tgg gat tat gtg acg gtc cgc aag gat gcc tac atg ttc tgg tgg
Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp
15 20 25
248
ctc tat tat gcc acc aac tcc tgc aag aac ttc tca gaa ctg ccc ctg
Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu
30 35 40 45
296
gtc atg tgg ctt cag ggc ggt cca ggc ggt tct agc act gga ttt gga
Val Met Trp Leu Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly
50 55 60
aac ttt gag gaa att ggg ccc ctt gag agt gat ctc aaa cca cgg aaa
Asn Phe Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys
65 70 75
344
acc acc tgg ctc cag gtc agt ctc cta ttt gtg gat aat ccc gtc
Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val
80 85 90
392
ggc act ggg ttc agt tat gtg aat ggt agt ggt gtc tat gcc aag gac
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp
95 100 105
440
ctg gtc atg gtg gct tca gag atq atg qtt ctc ctc aaq acc ttc ttc
488

```

Leu Ala Met Val Ala Ser Asp Met Met Val	Leu Leu Lys Thr Phe Phe		
110	115	120	125
agt tgc cac aaa gaa ttc cag aca gtt cca	tcc tac att ttc tca gag		536
Ser Cys His Lys Glu Phe Gln Thr Val Pro	Phe Tyr Ile Phe Ser Glu		
130	135	140	
tcc tat gga gga aat atg gca gct ggc	att ggt cta gag ctt tat aag		584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile	Gly Leu Glu Leu Tyr Lys		
145	150	155	
gcc att cag cga ggg acc atc aag tgc aac	ttt gcg ggg gtt gcc ttg		632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn	Phe Ala Gly Val Ala Leu		
160	165	170	
ggg gat tcc tgg atc tcc cct gtt gat tgc	gtg ctc tcc tgg gga cct		680
Gly Asp Ser Trp Ile Ser Pro Val Asp Ser	Val Leu Ser Trp Gly Pro		
175	180	185	
tac ctg tac agc atg tct ctt ctc gaa	gac aaa ggt ctg gca gag gtg		728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp	Lys Gly Leu Ala Glu Val		
190	195	200	205
tct aag gtt gca gag caa gta ctg aat	gcc gta aat aag ggg ctc tac		776
Ser Lys Val Ala Glu Gin Val Leu Asn Ala	Val Asn Lys Gly Leu Tyr		
210	215	220	
aga gag gcc aca gag ctg tgg ggg aat	gca gaa atg atc att gaa cag		824
Arg Glu Ala Thr Glu Leu Trp Gly Lys	Ala Glu Met Ile Glu Gln		
225	230	235	
gta aaa agg gga aac act gag cta gcc tgc	ttt gct ttt tct ggt		872
Val Lys Arg Gly Asn Thr Gln Arg Leu Ala	Cys Leu Ala Phe Ser Gly		
240	245	250	
ggg tac agg gcc cat ggt tgg tgt tgc	caa act tgg agt cta cac		917
Gly Tyr Arg Ala His Gly Trp Cys Gln	Thr Trp Ser Leu His		
255	260	265	
tgaggctccc cacatctcg caaatgttgc	catgttgtat aataaatctc ttgggtctaa		977
cgactgtatgt agtggctct tacagactca	aaaaggccacc caggctgcga agacttgctt		1037
gtcttcaact aatgttatgg	attctattaa aaaaaaaaaaaa aaaa		1081
<210> 4			
<211> 293			
<212> PRT			
<213> Homo sapiens			
<220>			

```

<400> 4
Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu Leu
-25 -20 -15
Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
-10 -5 1 5
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
10 15 20
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn
25 30 35
Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly
40 45 50
Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
55 60 65 70
Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu
75 80 85
Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser
90 95 100
Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val
105 110 115
Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr Val Pro
120 125 130

```

<210> 5
<211> 438
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5'UTR
<222> 1..83

<220>
<221> CDS
<222> 84..317

<220>
<221> 3'UTR
<222> 318..438

<220>
<221> polyA_signal
<222> 397..402

<220>
<221> polyA_site
<222> 423..438

gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161
Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His

-5 1 5
cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209

His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile
10 15 20

aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257
Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu

25 30 35 40
aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305

tca att gtc act tgatgata attgcaattt aaactgttaa gctgtgttca 357
Ser Ile Val Thr

60

gtactgtttc tgaataatag aaatcaatc tctaaaagca ataaatttca agacat	417
taataaaaaa aaaaaaaaaa a	438

<210> 6
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..19

<400> 6
Met Lys Phe Phe Val Phe Ala Leu Val Leu Ala Leu Met Ile Ser Met
-15 -10 -5
Ile Ser Ala Asp Ser His Glu Lys Arg His His Gly Tyr Arg Arg Lys
1 5 10
Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
15 20 25
Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
30 35 40 45
Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr
50 55

<210> 7
<211> 968
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..31

<220>
<221> CDS
<222> 32..748

<220>
<221> 3'UTR
<222> 749..968

<220>
<221> polyA_signal
<222> 928..933

<220>
<221> polyA_site
<222> 953..968

<400> 7
tgttcaggac tcctcagttc accttctcac a atg agg ctc cct gct cag ctc
Met Arg Leu Pro Ala Gln Leu 52
-15
Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
-10 -5 1 100
atg act cag tct cca ctc ttc ctg ccc gtc acc cct gga gag ccg gcc
Met Thr Gln Ser Pro Leu Phe Leu Pro Val Thr Pro Gly Glu Pro Ala
5 10 15 20 148
tcc atc tcc tgc agg tct agt cag agc ctc ctg cat gtt caa ggg tcc
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Val Gln Gly Ser
25 30 35 196

aac tat ttg gat tgg tac cac cag aag cca ggg cag tct cca caa ctc 244
 Asn Tyr Leu Asp Trp Tyr His Gln Lys Pro Gly Gln Ser Pro Gln Leu
 40 45 50
 ctg ata tac ttg ggt tct aat ccg gcc tcc ggg gtc cct gac agg ttc 292
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 55 60 65
 agt ggc agt gga tca ggc aca gat ttc aca ctg aaa atc agt aga gtg 340
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 70 75 80
 gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct cta caa act 388
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
 85 90 95 100
 cca ttc act ttc ggc cct ggg acc aga gtg gat atc aag cga act gtg 436
 Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
 105 110 115
 gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 484
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 120 125 130
 tct ggg act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 532
 Ser Gly Thr Ala Ser Val Cys Leu Asn Asn Phe Tyr Pro Arg
 135 140 145
 gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 580
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 150 155 160
 tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 628
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175 180
 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 676
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 185 190 195
 gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 724
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 200 205 210
 aag agc ttc aac agg gga gag tgt tagaggaga agtgccccca cctgtcttc 778
 Lys Ser Phe Asn Arg Gly Glu Cys
 215 220
 agttccagcc tgacccttc ccatctttg gcctctgacc cttttccac aggggaccta 838
 cccttatgc ggtcccccag ctcatcttc acctcacccc ccctcttc ctggcttta 898
 attatgtcaa ttgtggaga gaataataa ataaagtga tctttgcacc ttgtaaaaaa 958
 aaaaaaaaaa 968

<210> 8
 <211> 239
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<400> 8
 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Ser -5
 -20 -15 -10 -5
 Gly Ser Ser Gly Asp Ile Val Met Thr Gln Ser Pro Leu Phe Leu Pro
 1 5 10
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 15 20 25
 Leu Leu His Val Gln Gly Ser Asn Tyr Leu Asp Trp Tyr His Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Arg
 95 100 105
 Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 110 115 120
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 145 150 155
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 175 180 185
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 190 195 200
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 215

<210> 9
 <211> 730
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..730

<400> 9
 agatgagtgt tcagctcta gcagagagg tagctccct ctgcagcttg tcctgttgc 60
 tcctccaatgc tggtcgatgc cggagtttt atgagcctca gaggggagga agtgcatgtc 120
 gattaatcca tggcaggccc tgaaaaaggat ccactccag tctgcgggac ccacagctg 180
 gcccctcaggc tcaggccctt ccaggcctt agatgggc ttacacctggg actacccct 240
 tctgcctagg ago atg tot goc tcc tgc tcc ttc tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgg tcc ggc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634

cttggaaatg tagtagctt tattatccac atttgcaga tgaggaaaca gagtcaggtg 694
aagtgtctt tccaaggcca agctcctgag ggcagg 730

<210> 10
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..14

<400> 10
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
-10 -5 1
Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
5 10 15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
20 25 30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35 40 45 50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
55 60 65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
70 75 80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
85 90

<210> 11
<211> 733
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..253

<220>
<221> CDS
<222> 254..574

<220>
<221> 3'UTR
<222> 575..733

<400> 11
agatgagtgt tcagctctca gcagagaggt tagctctct ctgcagcttg tcctgttgtc 60
tcctcaagtc tggctgagtc cggagggtttt atggccctca gaaaaaggaa agtgcatgtc 120
gattaatccca tggcgaggcc ttggaaaatgg ccactccatc tctggggac ccacagctg 180
gccccctcgaggc ctcaaggccctt cccctggcttgg aagatggggc ttcaccttggg acctaccctt 240
tctgcctttagg agc atg ttt gcc tcc tgc ttt tca tgg tgc cca gcc 289
Met Ser Ala Ser Cys Leu Ser Trp Cys Pro Ala
-10 -5 1
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc ttt ggc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
1 5 10 15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac ttt 385
Ile His Cys Ile Ile Gly Arg Cys Asn Gly Phe Glu Asp Cys
20 25 30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
35 40 45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc ttt att gac aag agc 481

Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa ggt att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcataccctc ccagtaatcc ttgttatcgc 634
 ctttgaatg tagtagctt tattatccac attttgcaga tgaggaaaca gagtcaggcg 694
 aagtgtctt tccaaggcca agtcctgag ggcaggggc 733

<210> 12
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

<400> 12
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 13
 <211> 732
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..732

<400> 13
 agatgagtgt tcagctctca gcagagaggt tagctctctt ctgcagcttg tctgtttgtc 60
 tcctcaagtc tggtctgatc cgaggatttt atgagccatca gagggggaggaa agtgtcatgtc 120
 gatataatccca tggcaggccc tggaaaatgt cccactccag tctgcgggac ccacagcctg 180
 gcctctggc ctcaggccctt ccttggcttg aagatgggc ttcacctggg accataccct 240
 tctgcctagg agc atg tct gcc tcc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337

Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cggtcgcaatgggtttgagtgactgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctgttgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgc gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatacaccc tcggataatcc ttgttatcagc 634
 ctttgaaatg tagtagctt attatccaca ttttgcagat gaggaaacag agtcagggtga 694
 agtgtctttt ccaggccaa gtcctggagc gcaggggc 732

TOP STRAND: 5' UTR

<210> 14
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

<400> 14
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 15
 <211> 733
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..733

<400> 15
 agatgagtgt ttagcttctca gcagagagggt tagctccctct ctgcagcttg tcctgttgtc 60
 tcctcaagtc tggctgagtc cggagtttt atgacccctca gagggggagga agtgcatgtc 120
 gattaatcca tgggcaggcc tgaaaaagggtt ccactccag tcgtcgccgac ccacagccctg 180
 gcctctcaggc ytcaggccctt ccaggccctt aagatggggc ttacacctgg accatccccct 240
 ttcgccttagg agc atg tct gcc tcc tgc ttt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgc ttt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac ttt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc ttt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac ttt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt caa caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgaggcctga gctaattaag tgctggataa gcatcaccc ccagtaatcc tggatcagc 634
 ctttgaaatg tagtagttt tattatccac attttcaga tgaggaaaca gagtcagggt 694
 aagtgtcttt tccaaggcca agtcctgag ggcaggggc 733

<210> 16
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..14

<400> 16
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 17
<211> 1175
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..326

<220>
 <221> CDS
 <222> 327..1013

<220>
 <221> 3'UTR
 <222> 1014..1175

<220>
 <221> polyA_signal
 <222> 1131..1136

<220>
 <221> polyA_site
 <222> 1160..1175

<400> 17
 gaagcggagc ggtctaggga gccgcccc cgggtcaccc ggcgggtacg agttgttag 60
 ggtcacgtt acagcagcga cttagggctcg ggcgcggcg agatgcctt gttaccggc 120
 aacccttcg agcaagacgt ggtgtgccaa atgggtggaa aggagaaaat cacagaggaa 180
 taggttttttccatccaaat ttggtaacaaat ctaatttaaaat catagagact gggcggcgg 240
 ctgtggacaaat ttagatgtat atggatgtat atggtgggaa aatataaaaaat tcagagctg 300
 agcctgttta tatagatgtat gataatgtat gataga gccctgcaggtat cttcagg 353
 Met Asp Arg Ala Leu Gln Val Leu Gln
 1 5

agt	ata	gat	cca	aca	gat	tca	aaa	cca	gac	tcc	caa	gac	ctt	ttg	gat		401	
Ser	Ile	Asp	Asp	Pro	Thr	Asp	Ser	Lys	Pro	Asp	Ser	Gln	Asp	Leu	Leu	Asp		
10																		
tta	gaa	gat	atc	tgc	caa	cag	atg	ggt	cca	atg	ata	gat	gaa	aaa	ctt		449	
Leu	Glu	Asp	Ile	Cys	Gln	Met	Gly	Pro	Met	Ile	Asp	Glu	Lys	Leu				
gaa	gaa	att	gat	agg	aag	cat	tca	gaa	ttt	tct	gaa	ttt	aat	ttt	aaa		497	
Glu	Glu	Ile	Asp	Arg	Lys	His	Ser	Glu	Leu	Ser	Glu	Leu	Asn	Val	Lys			
gtc	ctg	gaa	gtt	ctg	gaa	cta	tat	aac	aaa	ttt	gtt	aat	gaa	gca	cca		545	
Val	Leu	Glu	Ala	Leu	Glu	Leu	Tyr	Asn	Lys	Leu	Val	Asn	Glu	Ala	Pro			
gtg	tac	tca	gtc	tat	tca	aag	ctc	cac	cct	cca	gca	cat	tac	cca	cct		593	
Val	Tyr	Ser	Val	Tyr	Ser	Lys	Leu	His	Pro	Pro	Ala	His	Tyr	Pro	Pro			
75																		
gca	tca	tct	ggg	gtt	cca	atg	cag	aca	tat	cca	gtt	caa	tca	cat	ggt		641	
Ala	Ser	Ser	Gly	Val	Pro	Met	Gln	Thr	Tyr	Pro	Val	Gln	Ser	His	Gly			
90																		
gga	aac	tat	atg	ggt	cag	agc	att	cac	caa	gta	act	ttt	gcc	caa	agc		689	
Gly	Aas	Tyr	Met	Gly	Gln	Ser	Ile	His	Gln	Val	Thr	Val	Ala	Gln	Ser			
110																		
tat	agc	cta	gga	ccc	gat	caa	att	ggt	cca	ctg	aga	tct	ctg	cct	cca		737	
Tyr	Ser	Leu	Gly	Pro	Asp	Gln	Ile	Gly	Pro	Leu	Arg	Ser	Leu	Pro	Pro			
125																		
aat	gtg	aat	tcc	tca	gtg	aca	gca	cag	cct	gtc	caa	act	tca	tat	tta		785	
Asn	Val	Asn	Ser	Ser	Val	Thr	Gln	Pro	Ala	Gln	Thr	Ser	Tyr	Leu				
140																		
agc	act	gga	caa	gac	act	gtt	tcc	aat	cct	act	tat	atg	aac	cag	aac		833	
Ser	Thr	Gly	Gln	Asp	Thr	Val	Ser	Asn	Pro	Thr	Tyr	Met	Asn	Gln	Asn			
155																		
tct	aac	cta	cag	tca	gtc	act	ggt	aca	act	gtt	tac	aca	cag	caa	atg		881	
Ser	Asn	Leu	Gln	Ser	Ala	Thr	Gly	Thr	Thr	Ala	Tyr	Thr	Gln	Gln	Met			
170																		
ggg	atg	tct	gtg	atg	tca	tct	tat	cag	aac	act	act	tcc	aat	ttt		929		
Gly	Met	Ser	Val	Asp	Met	Ser	Ser	Tyr	Gln	Asn	Thr	Thr	Ser	Asn	Leu			
190																		
cct	caa	ctg	gca	ggc	ttt	ccg	gtg	aca	gtt	cca	gct	cat	cca	gtt	gca		977	

Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
 205 210 215
 cag cag cac aca aat tac cat cag cag ctc ctt tagaaacaaa 1023
 Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
 220 225
 tcaaggattt ttttggaaagc ctccataact gtattattca gtccttgta taccacactg 1083
 aaaaatattaa aacttttttc cctctcaact caaaaggacc atgataaat aaagcacaaa 1143
 aacctctctt attctgaaaa aaaaaaaaaa at 1175

<210> 18
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Asp Arg Ala Leu Gln Val Leu Gln Ser Ile Asp Pro Thr Asp Ser
 1 5 10 15
 Lys Pro Asp Ser Gln Asp Leu Leu Asp Leu Glu Asp Ile Cys Gln Gln
 20 25 30
 Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
 35 40 45
 Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
 50 55 60
 Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
 65 70 75 80
 Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
 85 90 95
 Gln Thr Tyr Pro Val Gln Ser His Gly Asn Tyr Met Gly Gln Ser
 100 105 110
 Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
 115 120 125
 Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
 130 135 140
 Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
 145 150 155 160
 Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
 165 170 175
 Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
 180 185 190
 Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
 195 200 205
 Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
 210 215 220
 Gln Gln Pro Leu Leu
 225

<210> 19
 <211> 844
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..111

<220>
 <221> CDS
 <222> 112..813

<220>
 <221> 3'UTR
 <222> 814..844

TGGGG - UUUUUU660

<400> 19		
tttcctgttg ctgtctcta aacccttcca cattcccgcg gtccctcaga ctgccccggag	60	
agcgcgtct gcctgcgcc tgccctgcctg ccactgaggg ttcccagcac c atg agg	117	
Met Arg	-15	
gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc	165	
Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala		
-10	-5	1
cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act	213	
Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr		
5 10 15		
gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg	261	
Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val		
20 25 30		
gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg	309	
Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Val		
35 40 45 50		
gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg	357	
Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val		
55 60 65		
tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc	405	
Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro		
70 75 80		
acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat	453	
Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn		
85 90 95		
gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc	501	
Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Ala Thr Lys Cys		
100 105 110		
acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc	549	
Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile		
115 120 125 130		
ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa	597	
Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu		
135 140 145		
ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg	645	
Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu		
150 155 160		
tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg	693	
Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu		
165 170 175		
cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac	741	
Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp		
180 185 190		
cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg	789	
His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg		
195 200 205 210		
aag gcc aaa atc aag agt gag atg tagaaaatggtagaa aaagtggagt	843	
Lys Ala Lys Ile Lys Ser Glu Met		
215		
t	844	
<210> 20		
<211> 234		
<212> PRT		
<213> Homo sapiens		
<220>		
<221> SIGNAL		
<222> 1..17		
<400> 20		
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu		

-15 -10 -5
 Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
 1 5 10 15
 Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
 20 25 30
 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
 35 40 45
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
 50 55 60
 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
 65 70 75
 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
 80 85 90 95
 Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
 100 105 110
 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
 115 120 125
 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
 130 135 140
 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
 145 150 155
 Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
 160 165 170 175
 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
 180 185 190
 Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser
 195 200 205
 Ala Arg Lys Ala Lys Ile Lys Ser Glu Met
 210 215

<210> 21
 <211> 1997
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..126

<220>
 <221> CDS
 <222> 127..1020

<220>
 <221> 3'UTR
 <222> 1021..1997

<400> 21
 atcccttaag cttttaaata ttgcttcgtat ggtctgaatt tttatccaa gggaaaaaga 60
 gagtttgc ccacagtccag caggccacta gtttattaaac ttccagtcac ctgtatccc 120
 gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt ctg 168
 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Leu Val
 -15 -10 -5
 cct ctg ata aag cca gca cca acc cag gag gac tca cgc att atc 216
 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
 1 5 10
 tat gat tat gga aca gat aat ttt gaa gaa tcc ata ttt aca gat 264
 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp
 15 20 25
 tat gag tat gat aac tac ctg gat gga aaa aat att aag gaa aaa gaa act 312
 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr
 30 35 40
 qtg ata ata ccc aat qaq aaa aat ctt caa tta cca aaa qat qaq qca 360

卷之三

Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala
 45 50 55 60
 ata aca cca tta cct ccc aag aaa gaa aat gat gaa atg ccc acg tgt
 Ile Thr Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys
 65 70 75
 ctg ctg tgt gtt tta agt ggc tct gta tac tgt gaa gaa gtt gac
 Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp
 80 85 90
 att gat gct gta cca ccc tta cca aag gaa tca gcc tat ctt tac gca
 Ile Asp Ala Val Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala
 95 100 105
 cga ttc aac aaa att aaa aag ctg act gcc aaa gat ttt gca gac ata
 Arg Phe Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile
 110 115 120
 cct aac tta aga aga ctc gat ttt aca gga aat ttg ata gaa gat ata
 Pro Asn Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile
 125 130 135 140
 gaa gat ggt act ttt tca aaa ctt tct ctg tta gaa gaa ctt tca ctt
 Glu Asp Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu
 145 150 155
 gct gaa aat caa cta cta aaa ctt cca gtt ctt cct ccc aag ctc act
 Ala Glu Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr
 160 165 170
 tta ttt att gca aaa tac aac aaa atc aag agt agg gga atc aaa gca
 Leu Phe Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala
 175 180 185
 aat gca ttc aaa aaa ctg aat aac ctc acc ttc ctc tac ttg gac cat
 Asn Ala Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His
 190 195 200
 aat gcc ctg gaa tcc gtc cct ctt att tta cca gaa agt cta cgt gta
 Asn Ala Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val
 205 210 215 220
 att cat ctt cag ttc aac aac ata gct tca att aca gat gac aca ttc
 Ile His Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Phe
 225 230 235
 tgc aag gct aat gac acc agt tac atc cgg gac cgc att gaa gag ata
 Cys Lys Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile
 240 245 250
 cgc ctg gag ggc aat cca atc gtc ctg gga aag cat cca aac agt ttt
 Arg Leu Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe
 255 260 265
 att tgc tta aaa aga tta ccg at a ggg tca tac ttt 2aacctctat
 Ile Cys Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe
 270 275 280
 tggacttaaca tataaatgaa agtacaccta cactaatagt ctgtctcaac aatggataaa
 1090
 ggaacttaa tatttggtta atatttaaacct tttatgttcat tttttaaggaa ttatataattt
 1150
 taatcgaaagg tgttccaaat ctatccatata ataaatggaaa agtacatggact atgtctacg
 1210
 ttgtcaacaa ataaatgtaa ataaatttaa acgatccatc aaaaatccatg ttatatactg
 1270
 ataccatctt aataatccatg ttttttatgtaa atggccatcc ttgtatggatc attttctctt
 1330
 ttactaatg tgtaatggatc aggtatataatc acggaaactt tcaacttctt gcctttccgt
 1390
 gcttttactg gatccccaaa gatctttaagg tacatgttcc aaaaactttt aaaaagctaaa
 1450
 tggtttccatc gatgtccatc ttctttttttt tgatccatca gtatccatc ttatataatgg
 1510
 aactttttt tcccttccatc aaggccatctt ttttttatgtt ttttttttccatc agtccatgg
 1570
 atagcagata gtctcatat tagggaaactt ttccaataaa aataatgtt atttctgtat
 1630
 aaagcagata tacagaaatg ttcaatgtt ttatctttt ggtatgttcc ttatataatgg
 1690
 atttttttt tctaaatattt aacatcttacat gtcacccaaa aaaaatgtt aacttcaacga
 1750
 ggccaaaacc aataatgttca taagaaatata tggaaatgtt atccatctt gataaaatgg
 1810
 tctatggca agtctttcaaa atacgagata atcgagata aatccatctt tataatccat
 1870
 aataatggatc ctatcatca aattttgttca acgatccatg gaaacacaaatg tttatgttgg
 1930
 tggccatgttca cactacatctt ccacccatcatc acatccatgt tcaactgttac aacttcaat
 1990
 tccatcaaa
 1997

<211> 298
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..19

<400> 22
Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val Pro Leu
-15 -10 -5
Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile Tyr Asp
1 5 10
Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu
15 20 25
Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
30 35 40 45
Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr
50 55 60
Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu
65 70 75
Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp
80 85 90
Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe
95 100 105
Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn
110 115 120 125
Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp
130 135 140
Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu
145 150 155
Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe
160 165 170
Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala
175 180 185
Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala
190 195 200 205
Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His
210 215 220
Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys
225 230 235
Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu
240 245 250
Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe Ile Cys
255 260 265
Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe
270 275

<210> 23
<211> 1746
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..9

<220>
<221> CDS
<222> 10..1212

<220>
<221> 3'UTR

<222> 1213..1746

```
<220>
<221> polyA_signal
<222> 1709..1714
```

<220>
<221> polyA_site
<222> 1733 1746

Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
 255 260 265 270 915
 cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc
 Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
 275 280 285
 tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc
 Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
 290 295 300 963
 gct tgc cat gtc cac gat gag ttc agg acg gca gcg gtc gaa ggc cct
 Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
 305 310 315 1011
 ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca
 Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
 320 325 330 1059
 gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc
 Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
 335 340 345 350 1107
 gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc
 Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
 355 360 365 1155
 ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc
 Leu Arg Cys Leu Arg Gln His Asp Asp Phe Ala Asp Asp Ile Ser
 370 375 380 1203
 ctg ctg aag tgaggaggcc catggggcaga agataggat tcccctggac
 Leu Leu Lys 385 1252
 aaaaaaaaaaaa aaaa 1746

PROTEIN: CHICKEN

<210> 24
 <211> 401
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<400> 24
 Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly
 -15 -10 -5
 Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
 1 5 10 15
 Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
 20 25 30
 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ile Thr
 35 40 45
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
 50 55 60
 Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro
 65 70 75
 Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
 80 85 90 95
 Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
 100 105 110
 Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu

115	120	125
Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr		
130	135	140
Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met		
145	150	155
Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr		
160	165	170
Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser		175
180	185	190
Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu		
195	200	205
Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile		
210	215	220
Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser		
225	230	235
Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp		
240	245	250
Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser		255
260	265	270
Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val		
275	280	285
Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys		
290	295	300
His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val		
305	310	315
Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu		
320	325	330
Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu		335
340	345	350
Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg		
355	360	365
Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu		
370	375	380
Lys		
<210> 25		
<211> 1239		
<212> DNA		
<213> Homo sapiens		
<220>		
<221> 5'UTR		
<222> 1..126		
<220>		
<221> CDS		
<222> 127..879		
<220>		
<221> 3'UTR		
<222> 880..1239		
<220>		
<221> polyA_site		
<222> 1224..1239		
<400> 25		
agtcttagat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg	60	
gccaggagag tccccacagg agtgtcaagg ttcaatctca gcaccaagcca ctccagacgac	120	
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc	168	
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys		
-20	-15	-10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca	216	

Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
 -5 1 5
 ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca 264
 Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
 10 15 20
 gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat 312
 Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
 25 30 35
 ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
 Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
 40 45 50 55
 gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
 Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
 60 65 70
 tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
 Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
 75 80 85
 gag aac tgc agg ttccaa cac cag acg ctg gaa aac ggg tac gac gtc 504
 Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
 90 95 100
 tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
 Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
 105 110 115
 aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
 Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Tyr Ser Gln Phe Leu
 120 125 130 135
 tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
 Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
 140 145 150
 cgccgg cac acc cgg agc gcc gag gac tac tcg gag cgg gac ccc ctg 696
 Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
 155 160 165
 aac ggt ctg aag ccc cgg gcc cgg atg acc ccg gcc ccc tcc tgt 744
 Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
 170 175 180
 tca cag gag gtc ccc agc gcc gag gac aac agc ccg atg gcc agt gac 792
 Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
 185 190 195
 cca tta ggg gtc agg ggc ggt cga gtg aac agc cac gct ggg gga 840
 Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
 200 205 210 215
 acg ggc ccc gaa ggc tgc ccc ttc gcc aag ttc atc tagggcgt 889
 Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225
 ggaaggcac cctctttaac ccatccccca gcaaacgcac ctctcccaa ggaccaggtc 949
 cctctgacgtt ccggaggatgg gaaagggtt agggccatgt atggatttt ctgtttctct 1009
 ggggtccctt ccacaggagg ttcttgtaga accaaacctt gaggcccacat tcatgggtt 1069
 tcaccgcctt ctcactcca tatagaacac ctttcccaat aggaaccccc aacaggtaaa 1129
 cttagaaattt cccttcatg aaggttggaga gaagggtctt cttccaaat atttcttc 1189
 ctttgtcctt cttcttttat cacttttaag catggaaaaaaa aaaaaaaaaa 1239

<210> 26
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 26
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 -20 -15 -10

Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Asn Ser Pro Leu
 220 225

<210> 27
<211> 1179
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5'UTR
<222> 1..115

<220>
<221> CDS
<222> 116 961

<220>
<221> 3'UTR

<220>

<222> 1145..1150

<221> polyA_site
<222> 1164..1179

<400> 27
acaaattccc aatgca

```

cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa
Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln
166

```

5	10	15	
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt			214
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu			
20	25	30	
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag			262
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln			
35	40	45	
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga			310
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly			
50	55	60	65
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat			358
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr			
70	75	80	
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct			406
Cys Asp Met Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg Ser			
85	90	95	
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc			454
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly			
100	105	110	
ttt gga amt ttt gtccaa aat cat ggt gaa tat tgg ctg ggc aat aaa			502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys			
115	120	125	
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac			550
Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp			
130	135	140	145
ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc			598
Leu Ala Asp Phe GLy Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe			
150	155	160	
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat			646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr			
165	170	175	
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg			694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val			
180	185	190	
cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga			742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg			
195	200	205	
gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc			790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Glu Ser Gly			
210	215	220	225
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac			838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr			
230	235	240	
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc			886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr			
245	250	255	
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg			934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg			
260	265	270	
cca aat gat ttt att cca aat gta att taattgctgc tgttgggctt			981
Pro Asn Asp Phe Ile Pro Asn Val Ile			
275	280		
tcgtttctgc aattcagtt tgttaaagt gatttggaaa atactcattc tgaacatatac	1041		
catgcgcataat catgataact gtgttgagta gtgttttca ttcttcac ttgcctttgt	1101		
tacttaatgt gctttcagta cagcagatata gcaataataat gttagactgtg	1161		
tcaaaaaaaaaaaaaaaa aaaaaaaaaa	1179		

<210> 28
<211> 282
<212> PRT
<213> Homo sapiens

<220>

<221> UNSURE
<222> 116
<223> Xaa = Asn,Thr

<220>
<221> UNSURE
<222> 233
<223> Xaa = Phe,Ser

<400> 28
Met Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln
1 5 10 15
Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
20 25 30
Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
35 40 45
Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
50 55 60
Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
65 70 75 80
Tyr Cys Asp Met Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg
85 90 95
Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
100 105 110
Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
115 120 125
Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
130 135 140
Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
145 150 155 160
Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
165 170 175
Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
180 185 190
Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
195 200 205
Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
210 215 220
Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
225 230 235 240
Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
245 250 255
Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
260 265 270
Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
275 280

<210> 29
<211> 1118
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..344

<220>
<221> CDS
<222> 345..1118

<220>
<221> polyA_site
<222> 1103..1118

<400> 29
 aatccctagtc ttctgggttgc acgggttgcac tttttccata gcccagaggc cgagaggccc
 ttggccctgg gggaaaggagg acggaggttt ctgtggatcc cagcaggacg ctgtggcatt
 tggaaacaaa ggaatagtctt gcttggatcc ctggcagatc ttggggccgg aggccatgg
 aacccttggaa gcggaaaggaa gcaaggatgtt tcggaaacaa aactcgacgt gcttcagacg
 agcccccccgac tagctggaga ctccggccgc gacgtgtgcg ctgttctctt ggccagacg
 agccctttt gtgtctgggt taagagatt gtcccgatca tacc atg ggc cgc act
 Met Gly Arg Thr
 cgaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
 -15 -10 -5 1
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
 5 10 15
 atc tgg gag gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
 Ile Trp Asp Glu Asp Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
 20 25 30
 gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
 Gly Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
 35 40 45
 aaa ctt cag ggt gat tca gag gtc aag cct gag ggt agt ttg gga ctc 596
 Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
 50 55 60 65
 gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
 Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
 70 75 80
 gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
 Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
 85 90 95
 gaa cag gca agt gca aag gca ggc aac ggg gct agg gtt ggt acc atc 740
 Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
 100 105 110
 tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
 Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
 115 120 125
 ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
 Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
 130 135 140 145
 gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
 Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
 150 155 160
 cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
 Pro Ala Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
 165 170 175
 aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
 Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
 180 185 190
 atc ctg gag cga aca aat gat gat cct ttt att caa gaa gta gcc ttg gtc 1028
 Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
 195 200 205
 act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
 Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
 210 215 220 225
 gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa aaa
 Glu Leu Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys
 230 235

<210> 30

<210> 30

<212> PRT

<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..20

<220>
<221> UNSURE
<222> 49
<223> Xaa = Glu, *

<400> 30
Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile
-20 -15 -10 -5
Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp
1 5 10
Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
15 20 25
Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
30 35 40
Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
45 50 55 60
Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
65 70 75
Gly Ser His Ser Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
80 85 90
Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
95 100 105
Val Gly Thr Ile Ser Gly Asn Arg Thr Ile Ala Pro Ser Leu Pro Cys
110 115 120
Pro Gly Gly Arg Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
125 130 135 140
Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
145 150 155
Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
160 165 170
Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
175 180 185
Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
190 195 200
Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
205 210 215 220
Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
225 230 235
Lys Lys

<210> 31
<211> 1273
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..13

<220>
<221> CDS
<222> 14..1048

<220>
<221> 3'UTR
<222> 1049..1273

<220>
<221> polyA_signal

<222> 1234..1239

<220>
<221> polyA_site
<222> 1258..1273

<400> 31
 agagggttggg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
 -25 -20 -15
 tgc ggc cag gcg tgg ggt gcg tcg tgg ggc cgc agc tgc gag gag
 Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
 -10 -5 1
 ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac
 Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
 5 10 15 145
 ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt
 Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val
 20 25 30 35 193
 gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga
 Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg
 40 45 50 241
 agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc
 Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro
 55 60 65 289
 tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt
 Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe
 70 75 80 337
 aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg
 Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu
 85 90 95 385
 aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg
 Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu
 100 105 110 115 433
 gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac
 Asp Ser Ile Arg Pro Gln Lys Glu Gly Phe Arg Lys Glu Ile Asn
 120 125 130 481
 aag tgg tgg aat aac cta cta agt gat ggc cag egg act gtg aca ggt att
 Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
 135 140 145 529
 ata gct gca aat gtc ctt gta ttc ttt tga tgg aga gta cct tct ctg
 Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
 150 155 160 577
 cag cgg aca atg atc aga tat ttc aca tgg aat cca gcc tca aag qtc
 Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
 165 170 175 625
 ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt
 Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
 180 185 190 195 673
 cac atg gca gca aat agt tat gtt ttg tgg agc ttc tct tcc agc ata
 His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ile Ile
 200 205 210 721
 gtg aac att ctg ggt caa gag cag ttc atg gca gtc tac cta tct gca
 Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala
 215 220 225 769
 ggt gtt att tcc aat ttt gtc agt tac gtc ggt aaa gtt gcc aca gga
 Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly
 230 235 240 817
 aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg
 Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met
 245 250 255 865
 gat aca gca gga atg atc ctg gga tgg aaa ttt ttg gat cat ggc gca
 Asp Thr Ala Gly Met Ile Leu Gly Trp Lys Phe Asp His Ala Ala
 260 265 270 913

260 265 270 275
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat 961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His
280 285 290
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa 1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu
295 300 305
ata agg act aat ggc ccc aaa aaa gga ggt ggt tct aag taaaactggg 1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Ser Lys
310 315 320
atggacagt agtgttgcatt ctggtccttg ccgcctgaga gccccaggag acatcggtca 1118
gagtgaccat ggctatgctc ccgtctggaa gatgcacca tctgcctcc cactttttc 1178
agctgtgtcc cccagtcctg gtcttttag aatgtgaatg atgataaagt tgtgaaataa 1238
agtttttat ctatgttgc aaaaaaaaaaaaaaa 1273

<210> 32
<211> 345
<212> PRT
<213> Homo sapiens

2200
<221> SIGNAL
<222> 1..26

<400> 32
Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
-25 -20 -15
Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
-10 -5 1 5
Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
10 15 20
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
25 30 35
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
40 45 50
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
55 60 65 70
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
75 80 85
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
90 95 100
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
105 110 115
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
120 125 130
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
135 140 145 150
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
155 160 165
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
170 175 180
Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
185 190 195
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ile Val Asn Ile Leu
200 205 210
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
215 220 225 230
Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
235 240 245
Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
250 255 260
Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
265 270 275

Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
280 285 290
Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
295 300 305 310
Gly Pro Lys Lys Gly Gly Ser Lys
315

<210> 33
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..72

<220>
<221> CDS
<222> 73..672

<220>
<221> 3'UTR
<222> 673..723

<220>
<221> polyA_signal
<222> 689..694

<220>
<221> polyA_site
<222> 708..723

<400> 33
acaaagaaaag acatggctc agactgaagt accaactaa tcataccctt tcaaattttc 60
acggacacca tc atg gat tca aac acc gca cac agt ccg gtg ttt ctg gta 111
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val

1 5 10
ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser

15 20 25

gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg

30 35 40 45

aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr

50 55 60

ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro

65 70 75

agg ttt ccc ttt ata ttt tca gga tat cca ttc tgg ggc tct gtt 351
Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val

80 85 90

ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr

95 100 105

aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447
Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala

110 115 120 125

ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Thr Phe Gly Phe Ile Leu

130 135 140

gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

PROTEIN: Uncharacterized

145	150	155	
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc			591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe			
160	165	170	
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc			639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys			
175	180	185	
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tggtgagaata			692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys			
190	195	200	
aagatgtgtt aaaataaaaaaaa aaaaaaaaaaaa t			723

<210> 34
<211> 200
<212> PRT
<213> Homo sapiens

<400> 34			
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro			
1	5	10	15
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr			
20	25	30	
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys			
35	40	45	
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe			
50	55	60	
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro			
65	70	75	80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile			
85	90	95	
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr			
100	105	110	
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala			
115	120	125	
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn			
130	135	140	
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr			
145	150	155	160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile			
165	170	175	
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu			
180	185	190	
Asp Cys Asp Cys Glu Gln Cys Cys			
195	200		

<210> 35
<211> 845
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..118

<220>
<221> CDS
<222> 119..655

<220>
<221> 3'UTR
<222> 656..845

<220>

<221> polyA_signal

<222> 809..814

<220>

<221> polyA_site

<222> 830..845

<400> 35

acaaatagcc ccggatatct gtgttaccag ccttgtctcg gccaccta ggataatcac 60
taaattctgc caaaaggact gaggAACGGT gcctggaaaa gggcaagaat atcacggc 118
atg ggc atg agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt ttg atc tgt ggc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tcg ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtcttc cagaaaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgtataatc acagtaagaa gacttctgg 755
attatctctc tatcagatcaa gattttgtta atgtactatt ttactcttca ataaataaaa 815
cagttttta tcgaaaaaaaaa aaaaaaaaaa 845

<210> 36

<211> 179

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60

Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 Leu Leu Met Ser Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
 100 105 110
 Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
 115 120 125
 Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
 130 135 140
 Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
 145 150 155 160
 Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
 165 170 175
 Gly Pro Tyr

<210> 37
 <211> 517
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..16

<220>
 <221> CDS
 <222> 17..259

<220>
 <221> 3'UTR
 <222> 260..517

<400> 37
 ttccatagaa tggtag atg tca cca ggg cag cct atg aca ttc ccc cca gag 52
 Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu
 1 5 10
 gcc ctg tgg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
 Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
 15 20 25
 gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
 Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
 30 35 40
 gag gag aat gca gga gct gag gac cag gat ggg gag gga aaa ggc tcc 196
 Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
 45 50 55 60
 aag aca gcc ctg cag cct ctg aaa cac tac gac agc aaa gaa gat gat 244
 Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
 65 70 75
 gga caa gaa ata gcc tgccatgag gaccaggag ctgttacccc tccctacagc 299
 Gly Gln Glu Ile Ala
 80
 tcctaccctc tggctgaaat gggctgcac tggcggccct gcccccaaca gatgcattct 359
 gctctgacag gtggggctct tctccaaagg atgcgataca cagaccactg tgacggctta 419
 ttcttccaaat ggacatgatt cccaaatgtcat ctgtctgtct ttttttttat agacacaaatg 479
 aacagaccac ccacaacctt agttctctaa gtcatct 517

<210> 38
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 38

<210> 39
<211> 1816
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5' UTR
<222> 1..259

<220>
<221> CDS
<222> 260..1048

<220>
<221> 3'UTR
<222> 1049..1816

<220>
<221> polyA_signal
<222> 1782..1787

<220>
<221> polyA_site
<222> 1801..1816

```

<400> 39
actctggggc cattggccagc cggtctgttgc catttcgggc agttgtttttt gcatcttcata 60
ggaacctcg gaggcgccgc tccggcgctt ggttagcgaga ggccgggttcc ggatgtttccg 120
ggcttacttc gtcccaatgtt gtttaggggtt gatgtttttttt aatgtttttttt gatgtttttttt 180
aaatgttccat ccgtttttttttt ttggggccca ggccggatcc ttggccatccat cttttttttttttt 240
aaaggatgttc gtgtatcaga atg gtg tct gga cgg ttc tac ttt tcc tgc ctg 292
                                         Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu

```

-15 -10

ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340

Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
 -5 1 5
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met

ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
TTC AAC TGG CAC CCA GTG CTT ATG GTT GCT GGC ATG GTG GTA TTC TAT

```

Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
25                                30                                35                                40
gga ggt ggc tca ctg gtg tac cgc ctg ccc cag tcc tgg gtg ggg ccc
Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Glu Ser Trp Val Gly Pro
                                         484

```

```

        45          50          55
aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe

```

```

      60          65          70
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His
      75          80          85

```

gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc 628
 Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
 90 95 100
 act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ctg ggc ttt gct gtc ttc 676
 Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
 105 110 115 120
 ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc 724
 Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
 125 130 135
 cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc 772
 His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
 140 145 150
 att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc 820
 Ile Ser Ile Asn Glu Leu Phe Phe Ser Leu Lys Asn Thr Thr
 155 160 165
 agg cca tac cac agc ctg ccc agt gag ggc gtc ttt gcc aac agc acc 868
 Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
 170 175 180
 ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg 916
 Gly Met Val Val Ala Phe Gly Leu Val Leu Val Tyr Ile Leu Leu
 185 190 195 200
 gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag 964
 Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
 205 210 215
 ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac 1012
 Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
 220 225 230
 gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacactgtc 1058
 Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
 235 240
 tccaaagaac agagecctgtc cccagatgtc ccagtagcga tgtagtaacag aggtggctgt 1118
 ggacttcctc tactttctt tgctggatca gggtttctt gcctccccctt gggcaggctt 1178
 ggcttcctt ttgtggcagg gcccagcc ctctgaccac tctgcagotc acatgcagc 1238
 tgatgc当地 gtttgtgtgtt coagtgtgtca gcacccctgg gagccactgc cacccttcaga 1298
 ggggttctt tggtgagacc accatgtctt acctggccccc accatggctg ctggcctggc 1358
 ccaacctagc ttctctgtgcc atgttagaac tttagctgtt gctttttcttcc agggaggac 1418
 atagggtgga gagcggaaag ggttttgctt ctaagtgtt ctgtgtgtc ttttttgtt 1478
 ttcccaaaa acaactgtcca gggtccaaagc tttagactgc tggtgtttagt aagaactgt 1538
 gaagcttggg ttgtggagcc caccatctt ctggcagcat cagccatctt ctccctggca 1598
 catcaggcca acgtccaccc cagcttcaca ttggcagatg ttggcagaag ggctaattt 1658
 gaccgttttgg actgggttga ggcttcataagc caccatggat gtccctccagg cacctgggtc 1718
 ccatgaccag ctccccgtctt cccatgggtt aaggccatttca ctgggttatg aagctcgatg 1778
 ttcattaaat atgttaagaa tcaaaaaaaaaaaaaaaa 1816

<210> 40
 <211> 263
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<400> 40
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu Leu Leu Gly Ser Leu -5
 -20 -15 -10 -5
 Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg
 1 5 10
 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
 15 20 25
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
 30 35 40
 Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys

45 50 55 60
 Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
 65 70 75
 Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
 80 85 90
 Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
 95 100 105
 Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
 110 115 120
 Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
 125 130 135 140
 Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
 145 150 155
 Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
 160 165 170
 Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
 175 180 185
 Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
 190 195 200 200
 Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu
 205 210 215 220
 Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
 225 230 235
 Arg Gln Pro Tyr Lys Ser Trp
 240

 <210> 41
 <211> 643
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> 5'UTR
 <222> 1..90

 <220>
 <221> CDS
 <222> 91..462

 <220>
 <221> 3'UTR
 <222> 463..643

 <220>
 <221> polyA_signal
 <222> 607..612

 <220>
 <221> polyA_site
 <222> 628..643

 <400> 41
 accctaccc caccggccctt cccgcgcgcg cggttaatcc cccgcacctg agccatggct 60
 cacacctgca ccccgccccgg gcatagcacc atggccct gct tgg cgc ctt ggc ccg 114
 Met Pro Ala Cys Arg Leu Gly Pro
 -25
 cta gcc gcc gcc ctc ctc agc ctg ctg ttc ggc acc cta 162
 Leu Ala Ala Ala Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
 -20 -15 -10
 gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
 Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
 -5 1 5 10
 gct gac cag aac tgc acg caa gag tgc gtc tcg gac agc gaa tgc gcc 258

Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
 15 20 25
 gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
 Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
 30 35 40
 ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
 Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
 45 50 55
 cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgc tct 402
 Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
 60 65 70 75
 ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgc tct gtc 450
 Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
 80 85 90
 act ccc aat ttc tgtagctccag ccaccacca gctgagcagt gaggagagaaa 502
 Thr Pro Asn Phe
 95
 agtttctgcg tggccctgca tctggttcca gcgccacctgc cctccccc ttccggactc 562
 tggatccccctt ctggggctga ccacagcttc tcctttttttt aaccaataaa gtaaccactt 622
 tcacgaaaaaaaaaaaaaaa a 643

<210> 42
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..30

<400> 42
 Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser
 -30 -25 -20 -15
 Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
 -10 -5 1
 Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
 5 10 15
 Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
 20 25 30
 Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
 35 40 45 50
 Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
 55 60 65
 Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
 70 75 80
 Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
 85 90

<210> 43
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..227

<220>
 <221> CDS
 <222> 228..501

<400> 43
 actcttactc tttctctctc actctctctc tttccacc cttaaaggccaa gtacaggat 60

卷之三

<210> 44
<211> 91
<212> PRT
<213> *Homo sapiens*

<220>
<221> SIGNAL
<222> 1 .. 33

```

<400> 44
Met Gln Gly Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val
      -30          -25          -20
Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
      -15          -10          -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
      1           5           10          15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
      20          25          30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
      35          40          45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
      50          55

```

<210> 45
<211> 960
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5'UTR
<222> 1..97

<220>
<221> CDS
<222> 98 .. 934

<220>
<221> 3'UTR
<222> 935..960

<400> 45
ataatcacct ctcattccag actatgttag gcttaatgg tggaggacg cccgagtgtc 60
cgccccgtt caccggagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
Met Thr Pro Ser Glu Gly
1 5
gcc aga gca gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
10 15 20
gcc ttg ggc ggc ctg ctg ctt cggtt gat tcc gtg gag tgg gag ggg 211
Ala Leu Gly Gly Leu Val Leu Arg Asp Ser Val Glu Trp Glu Gly
25 30 35
cgc agt ctc ttg aag ggc ctt gtc aag aaa tct gca ctg tgg tgg gag 259
Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
40 45 50
caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Phe Arg Glu
55 60 65 70
gtt ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
75 80 85
aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Ala Phe Pro Gly Gly
90 95 100
ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
105 110 115
gtc acc att gct ctc gat tca ctc agg tgg ctg cta ctt cgc ctt ccc 499
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Arg Leu Pro
120 125 130
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gag tct 547
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
135 140 145 150
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
155 160 165
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
Leu His Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
170 175 180
ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcc 691
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
185 190 195
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac gag act 739
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr
200 205 210
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly
215 220 225 230
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccc gta 835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val
235 240 245
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt 883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly
250 255 260
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga 931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly
265 270 275
ttc tagggatggg gcagagtggc agcatac
Phe

<210> 46

<211> 279

<212> PRT

<213> Homo sapiens

<400> 46

Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu
1 5 10 15
Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val Leu Leu Arg Asp
20 25 30
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
35 40 45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
50 55 60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
65 70 75 80
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
85 90 95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
100 105 110
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
115 120 125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
130 135 140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Val Gly Lys
145 150 155 160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
165 170 175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
180 185 190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
195 200 205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
210 215 220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
225 230 235 240
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
245 250 255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
260 265 270
Trp Gly Trp Gly Gln Gly Phe
275

<210> 47

<211> 1294

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..266

<220>

<221> CDS

<222> 267..1139

<220>

<221> 3'UTR

<222> 1140..1294

<220>

<221> polyA_signal

<222> 1246..1251

<220>

<221> polyA_site

PROTEIN - UNPREDICTED

<400> 47
 gactctgagg ctcctcttt gctctaacag acacgacgca ctttaggctg gataatagt 60
 aaattttac ctgcgttctt cactgtatg agatctatg tgccgttttt tcagtttactc 120
 ttcaatggcc agtttttctga tctgttttca aaaaagaag tagagaatg aatctgttc 180
 ttcaataccat gaaaggaaaaa aaaaaataac ctcactccg tttttttttt aacattccaa 240
 gaacttcat cagagatccc acttag atg att tac aca atg aag aaa gta cat 293
 Met Ile Tyr Thr Met Lys Lys Val His
 -25 -20
 gca ctt tgg gct tct gta tgc ctg ctt aat ctt gcc cct gcc cct 341
 Ala Leu Trp Ala Ser Val Cys Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
 Leu Asn Ala Asp Ser Glu Glu Asp Glu His Thr Ile Ile Thr Asp
 1 5 10
 acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25 30
 gcg gat gat ggc cca tgc ttt aaa gca atc atg aaa aga ttt ttc ttc aat 485
 Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Asn
 35 40 45
 att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Cys Glu Gly
 50 55 60
 aat cag aat cga ctt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
 Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
 80 85 90
 cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
 Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
 95 100 105 110
 gaa cgt ttc aag tat tgt gga tgc ctg ggc aat atc aac aat ttt gag 725
 Glu Arg Phe Lys Tyr Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
 115 120 125
 aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
 Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
 130 135 140
 cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821
 Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Ser Leu
 145 150 155
 act ccg caa tca acc aag gtt ccc agg ctt ttt gaa ttt cac ggt ccc 869
 Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
 160 165 170
 tca tgg tgt ctc act cca gca gag aga gga ttg tgt cgt gcc aat gag 917
 Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
 175 180 185 190
 aac aca ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
 Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
 195 200 205
 tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa cca gaa 1013
 Tyr Ser Gly Cys Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
 210 215 220
 tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061
 Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
 225 230 235
 ggc cta att aaa acc aaa aga aaa aag aag cag aga gtc aaa ata 1109
 Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Arg Val Lys Ile
 240 245 250
 gca tat gaa gaa att ttt gtt aaa aat atg tgaatttgtt atagcaatgt 1159
 Ala Tyr Glu Glu Ile Phe Val Lys Asn Met

255 260
aacattaatt ctactaaata ttttatatga aatgtttcac tatgatttc tatgtttctt 1219
ctaaaatgct tttaataat atgttcattt aattttctat gcttattgtt 1279
aaaaaaaaaa aaaaa 1294

<210> 48
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..28

<400> 48
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
-25 -20 -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
-10 -5 1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5 10 15 20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
25 30 35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
40 45 50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
55 60 65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
70 75 80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85 90 95 100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
105 110 115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
120 125 130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
135 140 145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
150 155 160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165 170 175 180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
185 190 195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
200 205 210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
215 220 225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
230 235 240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245 250 255 260
Lys Asn Met

<210> 49
<211> 1194
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..47

<220>

<221> CDS
<222> 48..1100

<220>
<221> 3'UTR
<222> 1101..1194

<220>
<221> polyA_signal
<222> 1159..1164

<220>
<221> polyA_site
<222> 1179..1194

<400> 49
ctccctcagct tcaggccacca ccactgacctt gggacagtga atcgaca atg cgc tct 56
Met Pro Ser
tct gtc tgg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20 -15 -10 -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
1 5 10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
15 20 25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
30 35 40
cag ctg acc acc ggc aat ggc ctg ttc ctc aca gac gag ggc ctg aag cta 296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
45 50 55 60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
65 70 75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
80 85 90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
95 100 105
gat ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
110 115 120
aaa ggc aaa tgg gag aca ccc ttt gaa gtc aag gac acc gag gaa gag 536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu
125 130 135 140
gac ttc cac gtg gac gag gtg acc acc gtg aag gtg cct atg atg aag 584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
145 150 155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
160 165 170
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
175 180 185
cct gat gag ggg aaa cta cac cac ctg gaa aat gaa ctc acc cac gat 728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
190 195 200
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu
205 210 215 220

cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc 824
 His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val
 225 230 235
 ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc 872
 Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu
 240 245 250
 tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat 920
 Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His
 255 260 265
 aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc 968
 Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
 270 275 280
 atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag gtc aag ttc 1016
 Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe
 285 290 295 300
 aac aaa ccc ttt gtc ttc tta atg att gac caa aat acc aag tct ccc 1064
 Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro
 305 310 315
 ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa taactgcctc 1110
 Leu Phe Met Gly Lys Val Val Asn Pro Thr Glu Lys
 320 325
 tcgctctca acccctcccc tcacatccctg gccccctccc tgcatgcacat taaaagg 1170
 tttagctgaaa aaaaaaaaaaaaaaaa 1194

<210> 50
 <211> 351
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<220> 50
 Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
 -20 -15 -10
 Cys Leu Val Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 -5 1 5
 Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 10 15 20
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 25 30 35 40
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 45 50 55
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 60 65 70
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 75 80 85
 Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
 90 95 100
 Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
 105 110 115 120
 Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
 125 130 135
 Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro
 140 145 150
 Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu
 155 160 165
 Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile
 170 175 180
 phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu
 185 190 195 200
 Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser

205	210	215
Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu		
220	225	230
Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly		
235	240	245
Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys		
250	255	260
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala		
265	270	275
Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu		
285	290	295
Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr		
300	305	310
Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys		
315	320	325

<210> 51
<211> 1317
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..289

<220>
<221> CDS
<222> 290..1162

<220>
<221> 3'UTR
<222> 1163..1317

<220>
<221> polyA_signal
<222> 1269..1274

<220>
<221> polyA_site
<222> 1302..1317

<400> 51		
actctgccagt gatctctgaa gccgactctg aggctccctc ttgtctcaa cagacagca	60	
cgtactttagg ctgtataata gtccaaatttc tacctcgct tttcaactgct agtaaagatca	120	
gattcgctt ctttcagttt ctcttcaatc gcacgtttct tgatctgtttt cttaaaagaag	180	
aatgtatggaa gataaaatctt gtcttcaata ccgtggaaat gaaacaaaat aacctcaact	240	
ccgttttggaa aaaaacattc caagaacctt catcagatgttttacttag atg att tac	298	
Met Ile Tyr		
	-25	
aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ct	346	
Thr Met Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu		
-20	-15	-10
aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa	394	
Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu		
-5	1	5
cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat	442	
His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His		
10	15	20
tca ttt tgt gca ttc aag tcg gat gat ggc cca cca tgc aaa gca atc atg	490	
Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys Ala Ile Met		
25	30	35
aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata	538	
Lys Arg Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile		

45	50	55	
tat ggg gga tgt gaa gga aat cag aat cga ttt gaa agt ctg gaa gag Tyr Gly Gly Cys Glu Gly Asn Gln Arg Phe Glu Ser Leu Glu Glu	60	65	586
	70		
tgc aaa aaa atg tgt aca aga gaa aag cca gat ttc tgc ttt ttg gaa Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu	75	80	634
	85		
gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat aac Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn	90	95	682
	100		
aat cag aca aaa cag tag tga cgt ttc aag tat ggt gga tgc ctg ggc Asn Gln Thr Lys Glu Cys Arg Phe Lys Tyr Gly Cys Leu Gly	105	110	730
	115		
aat atg aac aat ttt gag aca ctg gaa gaa tgc aag aac att tgt gaa Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu	125	130	778
	135		
gat ggt ccg aat ggt ttc cag gtg gat aat tat gga acc cag ctc aat Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn	140	145	826
	150		
gct gtg aat aac tcc ctg act ccg caa tca acc aag gtt ccc agc ctt Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu	155	160	874
	165		
ttt gaa ttt cac ggt ccc tca tgg tgt ctc act cca gca gac aga gga Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly	170	175	922
	180		
ttg tgt cgt gcc aat gag aac aga ttc tac tac aat tca gtc att ggg Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly	185	190	970
	195		
aaa tgc cgc cca ttt aag tac agt gga tgt ggg gga aat gaa aac aat Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn	205	210	1018
	215		
ttt act tcc aaa caa gaa tgt ctg agg gca tgt aaa aaa ggt ttc atc Phe Thr Ser Lys Glu Cys Leu Arg Ala Cys Lys Lys Phe Ile	220	225	1066
	230		
caa aga ata tca aaa gga ggc cta att aaa acc aaa aga aaa aga aag Gln Arg Ile Ser Lys Glu Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys	235	240	1114
	245		
aag cag aga gtg aya ata gca tat gaa gaa att ttt gtt aaa aat atg Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met	250	255	1162
	260		
tgaatttttgtt atagcaatgt aacattaattt ctactaaat ttttatatgt aatgtttcac tatgatgttcc tatttttctt cttaaatgtct tttatataat atgttcatta aattttctat	25		1222
			1282
gcttatttgta ctgttatca aaaaaaaaaaaaaaaa aaaaaa aaaaaaaaaaaaaaaaaaaaaaa aaaaaa			1317

<210> 52
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..28

<400> 52
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
-25 -20 -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
-10 -5 1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5 10 15 20
Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
25 30 35
Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu

40 45 50
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
 55 60 65
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
 70 75 80
 Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
 85 90 95 100
 Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
 105 110 115
 Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
 120 125 130
 Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
 135 140 145
 Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
 150 155 160
 Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
 165 170 175 180
 Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
 185 190 195
 Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
 200 205 210
 Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
 215 220 225
 Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
 230 235 240 240
 Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
 245 250 255 260
 Lys Asn Met

<210> 53
 <211> 1907
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..1043

<220>
 <221> CDS
 <222> 1044..1664

<220>
 <221> 3'UTR
 <222> 1665..1907

<220>
 <221> polyA_signal
 <222> 1869..1874

<220>
 <221> polyA_site
 <222> 1892..1907

<400> 53
 caaaaaaaaatt cttaggtcatg atccccataa atgaagagtg atcagtccaa tccaggaa 60
 cctggacatt ttgggtattt ttcagtggaa acatgcctt cataaggttt atttcttg 120
 gtatcttta ggaagaacgc ataggaaaca ggcccatcg tctgcctgtt ttgccttc 180
 atctcacttc tacacgggg tgctgtgtt caattgtgtt tttcccataa agagacttt 240
 ttcacataatg ttgtgaaatg ccatcgacaa acctgtatgc attcgcatttc actctgtgt 300
 tgatgcattt ttctttttt ttatcatat ttaactatccctt gctctacaga gctttcacct 360
 tccacatattt tcagattcat tctttcttaa actatgtgtt ggctcacgtc ctcaactgact 420
 tatcaacatg ctaccatcat gcacttccata tctctatcc ttttttttaa attgggttcc 480

aatggctca caccattt ctgagctatt acctgcctac gcagtcctag aaagtaagt 540
 attcaggaaa cattcccaa aagtaaagt ttcaggtaa gatcagaaga ctcccatgag 600
 tcactgcgc tcaggatcac atctggctcc ttgaaggatg attccatcaga cttccatcatag 660
 atcttgcata aaaaatgaaa gagggctcgg gggaaaggctct tggtctgtg gttctgtg 720
 gagttccccc ttgtgggtt aaagocgttg cttagagct tcatcgccgg ttacttagt 780
 ttgtcttcgtt gtggacacggc catgcgttg cttcccccaaa gatcggaaa aattggcata 840
 gatggggccc ttcaaaaat cccactctgg gagcaactggc caaaattact accatctgt 900
 tgctgggtt ccgtttttt ccctttggaaat tataacatg gtccaaatttt aatggaaatgt 960
 ttcttcgttcc ttgttgcata atggagcaga acaaaatgtt aattttgcata 1020
 taaaatcttcc ttccagggtt gga atg cac ttc tgt gga ggc acc ttg ata tcc 1073
 Met His Phe Cys Gly Gly Thr Leu Ile Ser

1	5	10
---	---	----

cca gag tgg stg ttg act gct gcc cac tgc ttg gag aag tcc cca agg 1121
 Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg
 15 20 25

15	20	25
----	----	----

cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc 1169
 Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu
 30 35 40

30	35	40
----	----	----

gaa ccg cat gtt cag gaa ataa gaa gtg tct agg ctg ttc ttg gag ccc 1217
 Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro
 45 50 55

45	50	55
----	----	----

aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc 1265
 Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile
 60 65 70

60	65	70
----	----	----

act gac aaa gta atc cca gct ttt ctg cca tcc cca aat tat gtg gtc 1313
 Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val
 75 80 85 90

75	80	85	90
----	----	----	----

gct gac cgg acc gaa ttt ttc atc act ggc tgg gga gaa acc caa ggt 1361
 Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly
 95 100 105

95	100	105
----	-----	-----

act ttt gga gtc ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag 1409
 Thr Phe Gly Ala Gly Leu Leu Lys Ala Gln Leu Pro Val Ile Glu
 110 115 120

110	115	120
-----	-----	-----

aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc 1457
 Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser
 125 130 135

125	130	135
-----	-----	-----

acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag 1505
 Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln
 140 145 150

140	145	150
-----	-----	-----

ggt gac agt gga ggt ctt ctg gtt tgc ttc gag aag gac aat tac att 1553
 Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile
 155 160 165 170

155	160	165	170
-----	-----	-----	-----

tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag 1601
 Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys
 175 180 185

175	180	185
-----	-----	-----

cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga 1649
 Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly
 190 195 200

190	195	200
-----	-----	-----

gtg atg aga aat aat taatggacg ggagacagag tgacgcactg actcacctag 1704
 Val Met Arg Asn Asn
 205

205

aggctggaaac gtgggttaggg atttagctatg ctggaaataa ctggcgttta tccaaacgaaag 1764
 acactgtccc cagcttccatg ctatgccaa cctccggattttttgttta ttctgtactt 1824
 gtctggattct gtatgttggat gacatagctt tgacatgtttaaaaataaa ctctgtactt 1884
 aactttgaaa aaaaaaaaaaaa aaa 1907

<210> 54

<211> 207

<212> PRT

<213> Homo sapiens

<400> 54

Met His Phe Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr

1 5 10 15
 Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
 20 25 30
 Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
 35 40 45
 Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
 50 55 60
 Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
 65 70 75 80
 Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
 85 90 95
 Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
 100 105 110
 Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
 115 120 125
 Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
 130 135 140
 His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 145 150 155 160
 Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
 165 170 175
 Trp Gly Leu Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
 180 185 190
 Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 195 200 205

<210> 55
 <211> 809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..25

<220>
 <221> CDS
 <222> 26..628

<220>
 <221> 3'UTR
 <222> 629..809

<220>
 <221> polyA_signal
 <222> 766..771

<220>
 <221> polyA_site
 <222> 795..809

<400> 55
 agaaaagggtgt gggtggcatg gggca atg ctt gag gta tca gat gca ctg gga 52
 Met Leu Glu Val Ser Asp Ala Leu Gly
 1 5
 gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac 100
 Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp
 10 15 20 25
 acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148
 Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg
 30 35 40
 aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196
 Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro

TOSED2-UNSPEC2600

45	50	55	
ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc			244
Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser			
60	65	70	
ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg			292
Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val			
75	80	85	
tcc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca			340
Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala			
90	95	100	105
tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc			388
Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala			
110	115	120	
ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat			436
Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Asp			
125	130	135	
ctg cag agg atc atc ctg cga ctg ctg aac agt gat gag atg ttt gag			484
Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu			
140	145	150	
gac ctc ctg atg gag ctc acg aac cac qtc ctg agt gag tcg gat ctg			532
Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu			
155	160	165	
gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc			580
Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala			
170	175	180	185
aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc			628
Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys			
190	195	200	
tgatgttagcg gcaaataacct gacatggcg cctcgaggga gaccacagga atcgaacccc			688
cttcagact ggaggggat ggtttaagt atgactttgt actggggcca cactcacctc			748
tagaatattt ttattatag aaaaagaaaaa gcttttccctt agccccaaaa aaaaaaaaaa			808
t			809

<210> 56
<211> 201
<212> PRT
<213> Homo sapiens

<400> 56			
Met Leu Glu Val Ser Asp Ala Leu Gly Gly Pro Gly Arg Val Pro Gly			
1	5	10	15
Ala Thr Ala Gly Met Asn Gly Val Asp Thr Ser Leu Leu Cys Asp Leu			
20	25	30	
Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His			
35	40	45	
Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Tyr Lys Glu Ala			
50	55	60	
Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn			
65	70	75	80
Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe			
85	90	95	
Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala			
100	105	110	
Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn			
115	120	125	
Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg			
130	135	140	
Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr			
145	150	155	160
Asn His Val Leu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser			
165	170	175	
Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn			
180	185	190	

Ser Phe Arg Ile His Phe Trp Gly Cys
195 200

<210> 57
<211> 1133
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..475

<220>
<221> CDS
<222> 476..964

<220>
<221> 3'UTR
<222> 965..1133

<220>
<221> polyA_signal
<222> 1101..1106

<220>
<221> polyA_site
<222> 1118..1133

<400> 57
gacataaatca gagtatgtc ggaggagaag agggcagcca tttgttgctt ggcttcgtt
gaggcaggag gtgcaggac gagtttagag gctgtttag tagtcggc aagagcagg
ccccccaggag ttgtggggcc cccaggccc gcgggttcca gaggagacgc
aggaccccaa gtaactccg tgagaaggcg cgaccaggga ttcaaggcc agccaggctt
tccggggccca cgggttccc ctggattccc aggcaaaagggtt ggatcacccg gcccacccgg
ccctcaagca gagaaggcca gccaagggtat tcgaggccca tcaggccctgc ctggctccca
tgccggccaccc ggacccctcg ggattcaggg ccccgccgtt ctggatgttggatggaa
ggatggcaag cttgggttga gggggggggcc ttgttctgttggcccccgttggatggaa
gactc atg Met 60
1
gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
5 10 15
cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Thr Ser Gly Arg
20 25 30
cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
35 40 45
ggt ccc cgg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
50 55 60 65
cca gct ggg atc ttt gca gtg ggt ctg aaa gga gac cga gga gca acc 718
Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
70 75 80
gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
85 90 95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
100 105 110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccc ggt ccc atg ggc 862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
115 120 125

cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
 Gln Pro Gly Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
 130 135 140 145
 atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
 Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
 150 155 160
 ttg ggc tgaaatcccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
 Phe Gly
 ccaaaggctta taggactctg tgacaggttg tgaatgtttt ttttgttgg ttgttgttt 1074
 ttaattgtct ttaatatttt ttaataata aagaacaaa actaaaaaaa aaaaaaaaaa 1133

<210> 58
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro 1 5 10 15
 Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly 20 25 30
 Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg 35 40 45
 Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro 50 55 60
 Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala 65 70 75 80
 Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro 85 90 95
 Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro 100 105 110
 Met Gly Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met 115 120 125
 Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly 130 135 140 145
 Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly 150 155 160
 Pro Phe Gly

<210> 59
 <211> 838
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..78

<220>
 <221> CDS
 <222> 79..642

<220>
 <221> 3'UTR
 <222> 643..838

<220>
 <221> polyA_signal
 <222> 799..804

<220>
 <221> polyA_site
 <222> 823..838

<400> 59
aaagactgcg tgcagaagggt gactgtctca gtggagctgg gtcatctcg gccttggctc 60
cttgaacctt tgccccc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
1 5 10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
15 20 25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg acg ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
30 35 40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
45 50 55
gtt tat tat gag gag cag cac cca gag gtc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
60 65 70 75
gaa aca gag gga tta cgg tgc cga ggc aca aga tcc cct gtc ccc gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
80 85 90
gtt gag gat ccc gca acc gag gag cct ggg gag agg ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
95 100 105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
110 115 120
cac ggg gtt ctg gcc tgg gtc aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
125 130 135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
140 145 150 155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
160 165 170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
175 180 185
aaa tgaagatact gacaccaccc ttgccctccc cgtaacccgcg cacccacccct 692
Lys
gaccctcccc tca gctgtcc tggccccgc cctctcccgc acactcagtc cccctgcctg 752
gcgttctctgc cgcagctctg acctgggtgtt gtcgccttg catcttaata aamctctgtt 812
atatccct aaaaaaaaaaaaaaa 838

<210> 60
<211> 188
<212> PRT
<213> Homo sapiens

<400> 60
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1 5 10 15
Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
20 25 30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
35 40 45
Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
50 55 60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
65 70 75 80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
85 90 95

Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
 100 105 110
 Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
 115 120 125
 Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
 130 135 140
 Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
 145 150 155 160
 Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
 165 170 175
 Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
 180 185

<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..158

<220>
 <221> CDS
 <222> 159..764

<220>
 <221> 3'UTR
 <222> 765..862

<400> 61
 attttttttt ttggcacgcg tgcagccaa gttggggaggg ttccctggac agaggtcctt 60
 ttggctgtcg cttaagaact ggagcttggg ccgtggctgt cactgcgttc ggaccaggac 120
 ccgctgcagg cagcagcagc cccggccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Lys Glu Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agg gag gac tgc atc tcg cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tgg gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
 85 90 95
 gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
 100 105 110
 ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
 115 120 125 130

TUSSOO - Unchecked
 cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
 Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
 135 140 145
 ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
 Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
 150 155 160
 aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
 Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
 165 170 175
 ttc ggg atc gtg tagccgggg ggcggggggc gtggggggcc tggaggagg 804
 Phe Gly Ile Val
 180
 caggagccgc gggaggccgg gaggagggtg gggaccttc agccccatc ctctccgt 862

 <210> 62
 <211> 202
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

<400> 62
 Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
 -20 -15 -10
 Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
 -5 1 5 10
 Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
 15 20 25
 Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
 30 35 40
 Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
 45 50 55
 Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
 60 65 70 75
 Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
 80 85 90
 Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
 95 100 105
 Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
 110 115 120
 Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
 125 130 135
 Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
 140 145 150 155
 Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
 160 165 170
 Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
 175 180

<210> 63
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..194

 <220>
 <221> CDS
 <222> 195..587

<220>
<221> 3'UTR
<222> 588..618

<220>
<221> polyA_signal
<222> 578..583

<220>
<221> polyA_site
<222> 604..618

<400> 63
atttgcgttag gtctgatcaa tctgctccac acaaatttctc agtgatcctc tgcatctctg 60
cctacaaggg ctccttgcac accaaatgtca atattgtctca gaaacatgtca acttggatgtt 120
ttcggtttac ttctgatctct ctctgacaaa gaaatccaga tggatgcgaga cctgtatgtaa 180
acaatacatag gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu

-20 -15 -10

act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala

-5 1 5

cga cgt aag caa atg gaa atg cat atc tcc aga tac agt tca gaa caa 326
Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln

10 15 20

agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala

25 30 35

tat tca aca caa atg gag aga tcc aaa aga gat tac aca cca tca acc 422
Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr

40 45 50 55

act tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
Asn Ser Leu Ala Leu Ser Arg Ser Ile Ala Leu Pro Gln Gly Ser

60 65 70

atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg

75 80 85

act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met

90 95 100

tgc ttt gct tta cta aac tgt tagataatgt aagacgaaaa aaaaaaaaaa a 618
Cys Phe Ala Leu Leu Asn Cys

105 110

<210> 64
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..22

<400> 64
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
-20 -15 -10
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
-5 1 5 10
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
15 20 25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
30 35 40

<210> 65
<211> 836
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5'UTR
<222> 1..176

<220>
<221> CDS
<222> 177..767

<220>
<221> 3' UTR
<222> 768--836

<220>
<221> polyA_signal
<222> 814...819

<220>
<221> polyA_site
<222> 822..836

```
<400> 65
aatctgctec acgcaattc tcagtgatcc tctgcatac tgccatacg ggccttcctg 60
acacccaaatg tcatatgtc cagaacatgt gaacttgatgt ttttcatatcc accttggatct 120
ctctctgaca aagaatcca gatgtatcgat gacctgtatga agacaataca tggaaa atg 179
                                         Met
```

```

aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
-20          -15           -10          -5
ggc atc ctg gct att ttg tta aca aqa tqq qca cga cgt aag caa agt 275

```

```

gaa atg tat atc tcc aga tac agg tca gaa caa agg gct aga ctt ctg 323
  1          5          9          13         17          21         25
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser

```

```

Glu Met Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
15          20          25
gac tat gag pat ggt aga gga tcc cga cat gca tat tca aca caa act 371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Glu Ser

```

30	35	40	
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg			419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu			
45	50	55	60

```

tct cga tca agt att gct tta cct caa gga tcc atg agt agt agt ata aaa 467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
          65           70           75

tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515

```

```

Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
          80           85           90
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc      563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu

```

95 100 105

tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct			611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro			
110 115 120			
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc			659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu			
125 130 135 140			
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc			707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser			
145 150 155			
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt			755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu			
160 165 170			
ttc tcc cct get tgactccctc tcccttatgt gtaaaaacatt taaaaaatatg			807
Pho Ser Pro Ala			
175			
atagtgtata aatgaaaaaaaaaaaaaaaaaa			836

<210> 66

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..22

<400> 66

Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly			
-20 -15 -10			
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln			
-5 1 5 10			
Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu			
15 20 25			
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln			
30 35 40			
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala			
45 50 55			
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile			
60 65 70			
Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala			
75 80 85 90			
Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys			
95 100 105			
Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr			
110 115 120			
Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp			
125 130 135			
Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn			
140 145 150			
Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser			
155 160 165 170			
Leu Phe Ser Pro Ala			
175			

<210> 67

<211> 789

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..789

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 774..789

<400> 67
 atatgtcatc aggccccccg cctggggagggt gtgtgcacag agattttgc tcttcagggt 60
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtc agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg got gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggaggagcccccagggtggggagaaga gtctgcacagc agggctgtgg agttagggtt 652
 caccccaatggaccacccctctgggtccc ctgggtccgt ttttccttag aaatcagaga 712
 aatggaaaag gggggaaaac tgatTTACA cttaaaaaat aaaaatccat tagtaactcc 772
 gaaaaaaaaaaaaaa aaaaaaaaaaaaaaa 789

<210> 68
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 68

Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
 1 5 10 15
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 69
 <211> 2556
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..66

<220>
 <221> CDS
 <222> 67..2427

<220>
 <221> 3'UTR
 <222> 2428..2556

<220>
 <221> polyA_signal
 <222> 2522..2527

<220>
 <221> polyA_site
 <222> 2541..2556

<400> 69
 gtcccccgcgt ccttggcaat tcccgacttc ccaacggctt cctgtctggca gccccgaagc 60
 cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
 Met Phe Arg Leu Trp Leu Leu Ala Gly Leu Cys Gly Leu
 -15 -10 -5
 ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
 Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
 1 5 10 15
 cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat 204
 Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr
 20 25 30
 gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg 252
 Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val
 35 40 45
 cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg 300

His	Leu	Lys	Gln	Arg	Tyr	Phe	Leu	Thr	Asn	Phe	Met	Ile	Tyr	Leu		
50															60	
tac	aat	caa	gga	tct	atg	aat	act	tat	tct	tca	gat	att	cag	act	caa	348
Tyr	Asn	Gln	Gly	Ser	Met	Asn	Thr	Tyr	Ser	Ser	Asp	Ile	Gln	Thr	Gln	
65															75	
tgc	tac	tat	caa	gga	aat	att	gaa	gaa	tat	cca	gat	tcc	atg	gtc	aca	396
Cys	Tyr	Tyr	Gln	Gly	Asn	Ile	Glu	Glu	Tyr	Pro	Asp	Ser	Met	Val	Thr	
80															95	
ctc	agg	acg	tgc	tct	gga	cta	aga	gga	ata	ctg	caa	ttt	gaa	aat	gtt	444
Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg	Gly	Ile	Leu	Gln	Phe	Glu	Asn	Val	
100															110	
tct	tat	gga	att	gag	cct	ctg	gaa	tct	gca	gtt	gaa	ttt	cag	cat	gtt	492
Ser	Tyr	Gly	Ile	Glu	Pro	Leu	Glu	Ser	Ala	Val	Glu	Phe	Gln	His	Val	
115															125	
ctt	cac	aaa	tta	aag	aat	gaa	gac	aat	gat	att	gca	att	ttt	att	gac	540
Leu	His	Lys	Leu	Lys	Asn	Glu	Asp	Asn	Asp	Ile	Ala	Ile	Phe	Ile	Asp	
130															140	
aga	agc	ctg	aaa	gaa	caa	cca	atg	gat	gac	aac	att	ttt	ata	agt	gaa	588
Arg	Ser	Leu	Lys	Glu	Gln	Pro	Met	Asp	Asp	Asn	Ile	Phe	Ile	Ser	Glu	
145															155	
aaa	tca	gaa	cca	gct	gtt	cca	gat	tta	ttt	cct	ctt	tat	cta	gaa	atg	636
Lys	Ser	Glu	Pro	Ala	Val	Pro	Asp	Leu	Phe	Pro	Leu	Tyr	Leu	Glu	Met	
160															175	
cat	att	gtg	gtg	gac	aaa	act	ttg	tat	gat	tac	tgg	ggc	tct	gtt	agc	684
His	Ile	Val	Val	Asp	Lys	Thr	Leu	Tyr	Asp	Tyr	Trp	Gly	Ser	Asp	Ser	
180															190	
atg	ata	gtt	aca	aat	aaa	gtc	atc	gaa	att	gtt	ggc	ctt	gca	aat	tca	732
Met	Ile	Val	Thr	Asn	Lys	Val	Ile	Glu	Ile	Val	Gly	Leu	Ala	Asn	Ser	
195															205	
atg	tcc	ttc	acc	caa	ttt	aaa	gtt	act	att	gtg	ctg	tca	tca	ttg	gag	780
Met	Phe	Thr	Gln	Phe	Lys	Val	Thr	Ile	Val	Leu	Ser	Ser	Leu	Glu	Leu	
210															220	
tgg	tca	gat	gaa	aat	aag	att	tct	aca	gtt	ggt	gag	gca	gat	gaa	tta	828
Trp	Ser	Asp	Glu	Asn	Lys	Ile	Ser	Thr	Val	Gly	Glu	Ala	Asp	Glu	Leu	
225															235	
ttg	caa	aaa	ttt	tta	gaa	tgg	aaa	caa	tct	tat	ctt	aat	cta	agg	cct	876
Leu	Gln	Lys	Phe	Leu	Glu	Trp	Lys	Gln	Ser	Tyr	Leu	Asn	Leu	Arg	Pro	
240															255	
cat	gat	att	gca	tat	cta	att	tat	atg	att	gtat	cct	cgt	tat	ttg	924	
His	Asp	Ile	Ala	Tyr	Leu	Leu	Ile	Tyr	Met	Asp	Tyr	Pro	Arg	Tyr	Leu	
260															270	
gga	gca	gtg	ttt	cct	gga	aca	atg	tgt	att	act	cgt	tat	tct	gca	gga	972
Gly	Ala	Val	Phe	Pro	Gly	Thr	Met	Cys	Ile	Thr	Arg	Tyr	Ser	Ala	Gly	
275															285	
gtc	gca	ttg	tac	ccc	aag	gag	ata	act	ctg	gag	gca	ttt	gca	gtt	att	1020
Val	Ala	Leu	Tyr	Pro	Lys	Glu	Ile	Thr	Leu	Glu	Ala	Phe	Ala	Val	Ile	
290															300	
gtc	acc	cag	atg	ctg	gca	ctc	agt	ctg	gga	ata	tca	tat	gac	gac	cca	1068
Val	Thr	Gln	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	
305															315	
aag	aaa	tgt	caa	tgt	tca	gaa	tcc	acc	tgt	ata	atg	aat	cca	gaa	gtt	1116
Lys	Lys	Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	
320															330	335
gtg	caa	tcc	aat	ggt	gtg	aag	act	ttt	agc	agt	tgc	agt	ttg	agg	agc	1164
Val	Gln	Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Cys	Ser	Leu	Arg	Ser		
340															350	
ttt	caa	aat	ttc	aat	tca	aat	gtg	ggt	gtc	aaa	tgt	ctt	cag	aat	aag	1212
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
355															365	
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
370															380	
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggt	act	gag	gct	caa	tgt	gga	1308

Leu Glu Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly
 385 390 395 1356
 cct gca agc tgt ttt gat ttt cga act ttt gta ctg aaa gac gga gca
 Pro Ala Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala
 400 405 410 415
 aaa tgt tat aaa gga ctg tgc tgg aaa gac tgt caa att tta caa tca
 Lys Cys Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser
 420 425 430 1404
 ggc gtt gaa tgt agg ccc aaa gca cat cct gaa tgt gac atc gtc gaa
 Gly Val Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu
 435 440 445 1452
 aat tgt aat gga agc tca ccc gaa tgt ggt cct gac ata act tta atc
 Asn Cys Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile
 450 455 460 1500
 aat gga ctt tca tgc aaa aat aat aag ttt att tgt tat gac gga gac
 Asn Gly Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp
 465 470 475 1548
 tgc cat gat ctc gat gca cgt tgt gag agt gta ttt gga aaa ggt tca
 Cys His Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser
 480 485 490 495 1596
 aga aat gct cca ttt gcc tgc tat gaa gaa ata caa tct caa tca gac
 Arg Asn Ala Pro Phe Ala Cys Tyr Glu Ile Gln Ser Gln Ser Asp
 500 505 510 1644
 aga ttt ggg aac tgt ggt agg gat aga aat aac aaa tat gtg ttc tgt
 Arg Phe Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys
 515 520 525 1692
 gga tgg agg aat ctt ata tgt gga aga tta gtt tgt acc tac cct act
 Gly Trp Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr
 530 535 540 1740
 cga aag cct ttc cat caa gaa aat ggt gat gtt att tat gtc ttc gta
 Arg Lys Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val
 545 550 555 1788
 cga gat tct gta tgc ata acc gta gac tac aaa ttt cct cga aca gtt
 Arg Asp Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val
 560 565 570 575 1836
 cca gat cca ctg gct gtc aaa aat ggc tct cag tgt gat att ggg agg
 Pro Asp Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg
 580 585 590 1884
 gtt tgt gta aat cgt gaa tgt gta gaa tca agg ata att aag gct tca
 Val Cys Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser
 595 600 605 1932
 gca cat gtt tgt tca caa cag tgt tct gga cat gga gtt tgt gat tcc
 Ala His Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Val Cys Asp Ser
 610 615 620 1980
 aga aac aag tgc cat tgt tcg cca ggc tat aag cct cca aac tgc caa
 Arg Asn Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln
 625 630 635 2028
 ata cgt tcc aaa gga ttt tcc ata ttt cct gag gaa gat atg ggt tca
 Ile Arg Ser Lys Gly Ser Ile Phe Pro Glu Glu Asp Met Gly Ser
 640 645 650 655 2076
 atc atg gaa aca gca tct ggg aag act gaa aac acc tgg ctt cta ggt
 Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly
 660 665 670 2124
 ttcc ttc att gct ctt cct att ctc att gta aca acc gca ata gtt ttg
 Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Ala Ile Val Leu
 675 680 685 2172
 gca agg aca gag ttg aaa aac tgg ttc ggc aag gaa gag gaa ttc cca
 Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Phe Pro
 690 695 700 2220
 agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa
 Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln
 705 710 715 2268
 tcc acc tca gaa ggc agg act caq aca tat qcc gca cca acc aga tca
 2316

Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
 720 725 730 735 2364
 gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt
 Glu Ser Ser Ser Glu Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
 740 745 750 755 2412
 gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca
 Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
 755 760 765 770 2467
 caa agc agt aac tagtgattcc ttccagaaggc aacggataac atcgagagtc
 Gln Ser Ser Ser Asn 770 2527
 tcgctaagaa atgaaaatttc tgctttcct tcgcgttgtca cagctgaaag aaacaataaa 2556

<210> 70
 <211> 787
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16

<400> 70
 Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
 -15 -10 -5
 Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
 1 5 10 15
 Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
 20 25 30
 Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
 35 40 45
 Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
 50 55 60
 Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
 65 70 75 80
 Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
 85 90 95
 Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
 100 105 110
 Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
 115 120 125
 Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
 130 135 140
 Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
 145 150 155 160
 Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
 165 170 175
 Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
 180 185 190
 Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
 195 200 205
 Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
 210 215 220
 Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
 225 230 235 240
 Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
 245 250 255
 Ile Ala Tyr Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
 260 265 270
 Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
 275 280 285
 Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr

290	295	300
Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys		
305	310	315
Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln		320
325	330	335
Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln		
340	345	350
Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln		
355	360	365
Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu		
370	375	380
Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala		
385	390	395
Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys		400
405	410	415
Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val		
420	425	430
Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys		
435	440	445
Asn Gln Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gln		
450	455	460
Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His		
465	470	475
Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn		
485	490	495
Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe		
500	505	510
Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp		
515	520	525
Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys		
530	535	540
Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp		
545	550	555
Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp		
565	570	575
Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys		
580	585	590
Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His		
595	600	605
Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn		
610	615	620
Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg		
625	630	635
Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met		
645	650	655
Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu		
660	665	670
Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg		
675	680	685
Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Phe Pro Ser Ser		
690	695	700
Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser		
705	710	715
Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser		720
725	730	735
Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu		
740	745	750
Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser		
755	760	765
Ser Ser Asn		
770		

<211> 1603
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..7

<220>
<221> CDS
<222> 8..763

<220>
<221> 3'UTR
<222> 764..1603

<220>
<221> polyA_signal
<222> 1562..1567

<220>
<221> polyA_site
<222> 1588..1603

<400> 71
gagaagg atg ggg ccg cat cta cac ctg tgc ctg tgt gtg cct gac ctg 49
Met Gly Pro His Leu His Cys Leu Cys Val Pro Asp Leu
-15 -10 -5
cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97
Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
1 5 10
cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145
Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Lys Leu
15 20 25 30
ctg tac ctc tta gat ggg atg ctg gat ggg cag ctg aac agt ggt ata 193
Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
35 40 45
gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241
Ala Ala Thr Pro Ala Ser Ala Ala Ala Ala Thr Leu Asp Val Ala Val
50 55 60
cggtt ggc actt gtc tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289
Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
65 70 75
gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337
Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
80 85 90
tgg ctg aac atc agg ggc aag gag ggc gct gcc cta tcc atg ttc cat 385
Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His
95 100 105 110
gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433
Val Ser Thr Pro Leu Pro Val Met Thr Tyr Gly Phe Leu Ser Cys Ile
115 120 125
ttt ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481
Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
130 135 140
ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gat gca 529
Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala
145 150 155
ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc 577
Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Arg Val Leu Ala
160 165 170
ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg 625
Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg

175	180	185	190
gtg ctg aat gga gag gca cct cct agc cta ggc cct tcc tct gtg gcc			673
Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala			
195	200	205	
tcc cca gag gac gtc cag gcc ctg atg tac ctg aga ggg cag ctg gag			721
Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu			
210	215	220	
cct cag tgg aag atg ttg cag tgc cat cct cac ctg gtg gct			763
Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala			
225	230	235	
tggaaatcgcc caagggtggaa gcatttacac cgccggaaaatg acaccgcacg ccacgcggccc	823		
ggccgcgcga tcggaccccc aagccgcacgg ctccctcgac tctggggcac gaaacccgc	883		
ccactcccaa tcccccgcc ccgccttc ccacccgtgc ttcccccgct ccacccctca	943		
cctcaccctcg ccccgcccc accatcgcc ccccgccggc tggtattgtt cggtgggct	1003		
cggtcggcgg ctgtttccctc eggtctcgcc gggttcgttgtt cgttcggctt cctcacagcc	1063		
ccttcactccc ggccgtgtc agcagcagcgc gccggccggcgg gccgcgcctgc gggtttcgag	1123		
gctgagcggc tgggggggtt gggcggggag gaggagcagc acggggagga ggagccgtgt	1183		
gcccgtgcac tgagcggccg cggccatggc gtacgcctat ctcttcagt acatcataat	1243		
cggcgcacaca gggtttggta aatcatgtttt atgtctacag tttagacaca agaggttcag	1303		
cacatgtcatg accttactat tggtgttagag ttccgtgttc gaatgtataac tattgtatgg	1363		
aaacagataa aacttcagat atggatacg gcaggccaag aatccttcg ttccatcaca	1423		
aggtgttattt acagaggttc acggagactt ttactagttt acatattac acggagagat	1483		
acatccaacc acttgacaaac ctggtttagaa gatggccggcc agacattccaa ttccaacatg	1543		
gtcattatgc ttattggaaa taaaagtat ttagaatcta gaagaaaaaa aaaaagaaaa 1603			
<210> 72			
<211> 252			
<212> PRT			
<213> Homo sapiens			
<220>			
<221> SIGNAL			
<222> 1..17			
<220>			
<221> UNSURE			
<222> 173			
<223> Xaa = Ala,Gly			
<400> 72			
Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu Arg Ser			
-15	-10	-5	
Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro His Glu			
1	5	10	15
Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu Leu Tyr			
20	25	30	
Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile Ala Ala			
35	40	45	
Thr Pro Ala Ser Ala Ala Ala Ala Thr Leu Asp Val Ala Val Arg Arg			
50	55	60	
Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu Gly Gln			
65	70	75	
Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu Trp Leu			
80	85	90	95
Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His Val Ser			
100	105	110	
Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly			
115	120	125	
Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val			
130	135	140	
Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu			
145	150	155	
Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu			

160	165	170	175
Glu	Glu	Asn	Ser
Asn	Glu	Thr	Pro
Asn	Gly	Pro	Gln
Glu	Ala	Pro	Leu
Asp	Ala	Pro	Ala
Glu	180	185	190
Asp	195	200	205
Val	210	215	220
Trp	Lys	Met	Gln
	225	230	235
Trp	Lys	Leu	Cys
			His
			His
			Leu
			Val
			Ala

<210> 73
<211> 879
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..8

<220>
<221> CDS
<222> 9..395

<220>
<221> 3'UTR
<222> 396..879

<220>
<221> polyA_site
<222> 864..879

<400> 73	atg	gcc	gtg	ctg	ctg	ctg	ctc	cgt	gcc	ctc	cgc	cgg	ggf	50				
	Met	Ala	Val	Leu	Leu	Leu	Leu	Leu	Arg	Ala	Leu	Arg	Arg	Gly				
	-15							-10					-5					
	cca	ggc	ccg	ggf	cct	cgf	ccg	ctg	tgg	ggc	cca	ggc	ccg	gcc	ttg	agt	98	
	Pro	Gly	Pro	Gly	Pro	Arg	Pro	Leu	Trp	Gly	Pro	Gly	Pro	Ala	Trp	Ser		
	1														15			
	cca	ggg	ttc	ccc	gcc	agg	ccc	ggg	agg	ggg	ccg	ccg	tac	atg	gcc	agc	146	
	Pro	Gly	Phe	Pro	Ala	Arg	Pro	Gly	Arg	Gly	Arg	Pro	Tyr	Met	Ala	Ser		
								20			25			30				
	agg	cct	ccg	ggg	gac	ctc	gcc	gag	gtt	ggg	ggc	cga	gct	ctg	cag	agc	194	
	Arg	Pro	Pro	Gly	Asp	Leu	Ala	Glu	Ala	Gly	Gly	Arg	Ala	Leu	Gln	Ser		
								35			40			45				
	tta	caa	ttg	aga	ctg	cta	acc	cct	acc	ttt	gaa	ggg	atc	aac	gga	ttg	242	
	Leu	Gln	Leu	Arg	Leu	Leu	Thr	Pro	Thr	Phe	Glu	Gly	Ile	Asn	Gly	Leu		
								50		55			60					
	ttg	tta	aaa	caa	cat	tta	gtt	cag	aat	cca	gtc	aga	ctc	tgg	caa	ctt	290	
	Leu	Lys	Gln	His	Leu	Val	Gln	Asn	Pro	Val	Arg	Leu	Trp	Gln	Leu			
								65		70			75					
	tta	ggf	ggf	act	ttc	tat	ttt	aac	acc	tca	agg	ttg	aag	cag	aat		338	
	Leu	Gly	Gly	Thr	Phe	Tyr	Phe	Asn	Thr	Ser	Arg	Leu	Lys	Gln	Asn			
								80		85			90					
	aag	gag	aag	gtt	tcg	aag	ggg	aag	ggc	cct	gaa	gag	gac	gaa	ggf		386	
	Lys	Glu	Lys	Asp	Lys	Ser	Lys	Gly	Lys	Ala	Pro	Glu	Asp	Glu	Gly			
								100		105			110					
	ata	tcc	atc	tgtatgttctt	cagt	cagt	tag	ctgc	cct	tgg	atgt	cttttac					435	
	Ile	Phe	Ile															
	rttttgttt	wcc	ttttggc	aagg	ttttggaa	ac	gtt	ttttgggg	495									
	gcagtggc	tc	acat	ttgtt	aa	tcg	aa	acgt	ttgg	agg	cc	cagg	ttgg	aa	gg	ttgg	555	
	ggc	c	c	ttat	acc	acat	gtt	c	ttt	gg	gg	ttt	gg	ttt	gg	ttt	615	
	tc	ac	ac	cc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	675	
	ca	ac	at	gtt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	735	

gcctgtataatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctggggaggtg 795
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaaac 855
tccatcccaa aaaaaaaaaaaa aaaa 879

<210> 74
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..16

<400> 74
Met Ala Val Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly Pro Gly
-15 -10 -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
1 5 10 15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
20 25 30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
35 40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
50 55 60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65 70 75 80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
85 90 95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
100 105 110
Ile

<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..87

<220>
<221> CDS
<222> 88..1269

<220>
<221> 3'UTR
<222> 1270..1634

<220>
<221> polyA_signal
<222> 1594..1599

<220>
<221> polyA_site
<222> 1619..1634

<400> 75
aaagttcctc agcccttggc tcctgccag tggtaggggt gtggccggag acaaaaggaa 60
agagtcatcg cctgtcgaaa cttagat atg atg ggt gtg ttt gta gtt gct gct 114
Met Met Gly Val Phe Val Val Ala Ala
1 5
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162

Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
 10 15 20 25
 gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
 Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
 30 35 40
 aaa gtc tca cct gaa aca gtt gac agt gtc att atg ggc aat gtc ctg 258
 Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
 45 50 55
 cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306
 Gln Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg
 60 65 70
 gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354
 Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys
 75 80 85
 ggt tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402
 Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val
 90 95 100 105
 aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450
 Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln
 110 115 120
 gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498
 Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser
 125 130 135
 gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat 546
 Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His
 140 145 150
 gtc cag ctc ccc atg gca atg act gca gag aat ctt gtc gta aaa cac 594
 Val Gln Leu Pro Met Ala Thr Ala Glu Asn Leu Ala Val Lys His
 155 160 165
 aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag 642
 Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln
 170 175 180 185
 aga tgg aaa gct gat gat gat gct ggc tac ttt aat gat gaa atg gca 690
 Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala
 190 195 200
 cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac 738
 Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp
 205 210 215
 gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct 786
 Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro
 220 225 230
 cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tcg ggt 834
 Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly
 235 240 245
 gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt 882
 Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val
 250 255 260 265
 aag aaa cat aac ttc aca cca ctg gca aga att gtt ggc tac ttt gta 930
 Lys Lys His Asn Phe Thr Pro Leu Ala Arg Ile Val Gly Tyr Phe Val
 270 275 280
 tct gga tgt gat ccc tct atc atg ggt att ggt cct gtc cct gct atc 978
 Ser Gly Cys Asp Pro Ser Ile Met Gly Ile Gly Pro Val Pro Ala Ile
 285 290 295
 agt ggg gca ctg aag aaa gca gga ctg agt ctt aag gac atg gat ttg 1026
 Ser Gly Ala Leu Lys Lys Ala Gly Leu Ser Leu Lys Asp Met Asp Leu
 300 305 310
 gta gag gtc aat gaa gct ttt gct ccc cag tac ttg gct gtt gag agg 1074
 Val Glu Val Asn Glu Ala Phe Ala Pro Gln Tyr Leu Ala Val Glu Arg
 315 320 325
 agt ttg gat ctt gac ata agt aaa acc aat gtc aat gga gga gcc att 1122
 Ser Leu Asp Leu Asp Ile Ser Lys Thr Asn Val Asn Gly Gly Ala Ile
 330 335 340 345
 gct ttg ggt cac cca ctg gga gga tct gga tca aga att act gca cac 1170

```

Ala Leu Gly His Pro Leu Gly Gly Ser Gly Ser Arg Ile Thr Ala His
      350          355          360
ctg gtt cac gaa tta agg cgt cga ggt gaa aaa tat gcc gtt gca tca 1218
Leu Val His Glu Leu Arg Arg Arg Gly Gly Lys Tyr Ala Val Gly Ser
      365          370          375
gct tgc att gga ggt ggc caa ggt att gtc atc att cag agc aca 1266
Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr
      380          385          390
gcc tgaagagacc agtgagctca ctgtgaccca tccttactct acttggccag 1319
Ala
gcccacgat aaacaagtgtac cttagagac gtcgtccaaat ctggccatgc cctggccattg 1379
aaacacgtat taaggtttat caaaggcatgg tgacaaaaaa atgcattgtat catgaatagg 1439
ggcccatgtc aaagaatgtat ttcttcatgt ttgaaccatgg gaaatatgtat gtatttctgt 1499
gtctaaatcc aactatagaa gacataaaaaa gaaatcgat tcttgcggaa taaccaccc 1559
tttgtccatata gataatatgttataaaggaa atcaaaaatggaa ttatggccatgttacttgc 1619
aaaaaaaaaaaa 1634

```

```

<210> 76
<211> 394
<212> PRT
<213> Homo sapiens

<400> 76
Met Met Gly Val Phe Val Val Ala Ala Lys Arg Thr Pro Phe Gly Ala
1 5 10 15
Tyr Gly Gly Leu Leu Lys Asp Phe Thr Ala Thr Asp Leu Ser Glu Phe
20 25 30
Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro Glu Thr Val
35 40 45
Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile
50 55 60
Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr
65 70 75 80
Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile
85 90 95
Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu
100 105 110
Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn
115 120 125
Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser
130 135 140
Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met
145 150 155 160
Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Cys
165 170 175
Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp
180 185 190
Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys
195 200 205
Lys Gly Lys Gln Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr
210 215 220
Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly
225 230 235 240
Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala
245 250 255
Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro
260 265 270
Leu Ala Arg Ile Val Gly Tyr Phe Val Ser Gly Cys Asp Pro Ser Ile
275 280 285
Met Gly Ile Gly Pro Val Pro Ala Ile Ser Gly Ala Leu Lys Lys Ala
290 295 300
Gly Leu Ser Leu Lys Asp Met Asp Leu Val Glu Val Asn Glu Ala Phe
305 310 315 320

```

Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser
325 330 335

Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly
340 345 350

Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg
355 360 365

Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gln
370 375 380

Gly Ile Ala Val Ile Ile Gln Ser Thr Ala
385 390

<210> 77

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..68

<220>

<221> CDS

<222> 69..875

<220>

<221> 3'UTR

<222> 876..1642

<220>

<221> polyA_signal

<222> 1599..1604

<220>

<221> polyA_site

<222> 1627..1642

<400> 77

attttatacg gcgcgcgggc gcgcgcggca gcgggttggag gttttaggac cggcggggaa 60
taggaatc atg gcg gct gct ctg ttc gtg ctg ctg gga ttc gcg ctg ctg 110
Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
-20 -15 -10

ggc acc cac gga gcc tcc ggg gct gcc ggc aca gtc ttc act acc gta 158
Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
-5 1 5 10

gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc 206
Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
15 20 25

gcc aca gag stc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg 254
Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Val Val Leu
30 35 40

aag gag gac ggc ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc 302
Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
45 50 55

gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg 350
Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
60 65 70

ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
75 80 85 90

aag tcg tca gaa cac atc aac gag ggg gag acg goc atg ctg gtc tgc 446
Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
95 100 105

aag tca gag tcc gtg cca cct gtc act gag tgg gcc tgg tac aag atc 494

Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile
 110 115 120 542
 act gac tct gag gac aag gcc ctc atg aac ggc tcc gag agc agg ttc
 Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe
 125 130 135 590
 ttc gtg agt tcc tcg cag ggc ctg tca gag cta cac att gag aac ctg
 Phe Val Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu
 140 145 150 150 638
 aac atg gag gcc gac ccc ggc gag tac cgg tgc aac ggc acc agc tcc
 Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser
 155 160 165 170 686
 aag ggc tcc gac cag gcc atc atc acg ctc cgc gtg cgc agc cac ctg
 Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu
 175 180 185 185
 gcc gcc ctc tgg ccc ttc ctg ggc atc gtg gct gag gtg ctg gtg ctg
 Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu
 190 195 200 734
 gtc acc atc atc ttc atc tac gag aag cgc cgg aag ccc gag gag gtc
 Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val
 205 210 215 782
 ctg gat gat gac gac gcc ggc tct gca ccc ctg aag agc agc ggg cag
 Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln
 220 225 230 830
 cac cag aat gac aaa ggc aag aac gtc cgc cag agg aac tct tcc
 His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
 235 240 245 875
 tggaggcagggtggccgggaa cgtcccttcgc tcccggtctgc cgccggccggc ggaggccact 935
 ccccaagtgttgc gaaaggattcc aagtttctcac ctctttaaaga aaaccacccc cgttagattcc 995
 catcatatacac ttccctttttt ttaaaaaaaaat ttgggttttc tccattcagg attttgttcc 1055
 tttaggtttt ttcccttgcg aagtgtttcac gagagccccgg gaggctgtgc cctgcggccc 1115
 cgtctgttggc ttccacgttc tggttgcgatg tcatggccgg gtggggcgca cagcccttcc 1175
 cactggccgg agtcagtgcc aggttcttcgc ecctttgtgg aagtccacagg tcacacagggg 1235
 ggccccgtgt tgactgttgc tgaaaggccat gtctgttgc tgcccatttt ttgtgttttt 1295
 atgtttaattt ttagggggc cacgggtctg tggttgcactc agccctcaggg acgactctga 1355
 cctcttgccca acagaggact cacttgcggcca caccggggc gaccggctca cagccctcaag 1415
 tcaactcccaa gccccctctt tgctgtgca tccggggggca gctctggagg gggtttgtg 1475
 gggaaactggc gccatcgccg ggactccaga accggagaag cctcccccgc tcacccctgg 1535
 aggacacggc ggtctctata gcaaccgggc taatgtggg accccccctcc caccacccgc 1595
 cacaataaaag atgcggccca ctccacccctt caaaaaaaaaaaaaaaa 1642

<210> 78
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

<400> 78
 Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr
 -20 -15 -10
 His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
 -5 1 5 10
 Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
 15 20 25
 Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
 30 35 40
 Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
 45 50 55
 Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
 60 65 70 75
 Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser

	80	85	90
Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser			
95	100	105	
Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp			
110	115	120	
Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val			
125	130	135	
Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met			
140	145	150	155
Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly			
160	165	170	
Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala			
175	180	185	
Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr			
190	195	200	
Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp			
205	210	215	
Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln			
220	225	230	235
Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser			
240	245		

<210> 79
<211> 1466
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..343

<220>
<221> CDS
<222> 344..1144

<220>
<221> 3'UTR
<222> 1145..1466

<400> 79			
atttgtactt tggccaggc tggggaaat gaccgggg ggtcccatgc ggctacataaa	60		
aattggcaggc tttagaacta gtggaaaggc gggtgcgcga agtcgagggg cgagagagg	120		
ggggccggagg agctgttttc tgaaatccaag ttctgtggct ctctcagaag tccttcggac	180		
ggggcggagg tggccggcgcc gcccggctta ctgcgcctyt gccttccttc cataaccttt	240		
tcttttcggac tcaaatcaacg gctgtcgca agggctctagt tcggacact agggtgcccg	300		
aacgcgcgtgtc tgcccgaggt gtcgcgggg cttccggcta acc atg ctg ccg ccg	355		
Met Leu Pro Pro			
ccg ccg ccc gca gct gcc ttg gcg ctg cct gtg ctc cta ctg ctg	403		
Pro Arg Pro Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu			
-25 -20 -15 -10			
gtg gtg ctg acg ccc ccg acc ggc gca agg cca tcc cca ggc cca	451		
Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro			
-5 1 5			
gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc	499		
Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Ala Glu Gly Glu Gly			
10 15 20			
tgc gct ccc tgc cgg cca gaa gag gac ggc tgc ggc cgg ggc tgc ctg	547		
Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu			
25 30 35			
gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgg gaa tgc gcc aac	595		
Ala Gly Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn			
40 45 50 55			
ctc gag ggc cag ctc tgc gac ccc agt gct cac ttc tac ggg	643		

Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala His Phe Tyr Gly
 60 65 70
 cac tgc ggc gag ctt gag tgc cgg ctg gac aca ggc ggc gac ctg
 His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr Gly Gly Asp Leu
 75 80 85
 agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgc cgt tcg cag agt
 Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys Arg Ser Gln Ser
 90 95 100
 ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag atc tgc cgc ctg
 Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln Ile Cys Arg Leu
 105 110 115
 cag gag gcg gcc cgc gct cgg ccc gat gcc aac ctc act gtg gca cac
 Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu Thr Val Ala His
 120 125 130 135
 ccg ggg ccc tgc gaa tcg ggg ccc cag atc gtg tca cat cca tat gac
 Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser His Pro Tyr Asp
 140 145 150
 act tgg aat gtg aca ggg cag gat gtg atc ttt ggc tgt gaa gtg ttt
 Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly Cys Glu Val Phe
 155 160 165
 gcc tac ccc atg gcc tcc atc gag tgg agg aag gat ggc ttg gac atc
 Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu Asp Ile
 170 175 180
 cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg ggt gga
 Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly
 185 190 195
 ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct gtg cgt
 Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg
 200 205 210 215
 ccc agt gat gag ggc act tac cgc tgc ctt ggc cca atg ccc tgg gtc
 Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro Met Pro Trp Val
 220 225 230
 aag tgg agg ccc ctg cta gct tgacagtgtc cacacctgac cagctgaact
 Lys Trp Arg Pro Leu Leu Ala
 235
 ctacaggcat ccccccacgtg cgatcaactaa acctgggttcc tgaggaggag gctgagagtg
 aagagaatga cgattactac taggtccaga gctctggccc atgggggtgg gtgagcggct
 atatgttgtca tcctctgtct tgaaaaagacc tgaaaagggg agcggggctc ctccatcgac
 tgctttcatg ctgtcaatg ggtatgtatc ggaggcccta ttgtactcca aggttagcagt
 gtggtaggat agagacaaaa gctggaggag ggttagggaga gaagctgaga cc
 1234
 1294
 1354
 1414
 1466

<210> 80
 <211> 267
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..30

<400> 80
 Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu
 -30 -25 -20 -15
 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro
 -10 -5 1
 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
 5 10 15
 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
 20 25 30
 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp
 35 40 45 50
 Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
 55 60 65

His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
 70 75 80
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
 85 90 95
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
 100 105 110
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
 115 120 125 130
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
 135 140 145
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
 150 155 160
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 165 170 175
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 180 185 190
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 195 200 205 210
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
 215 220 225
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
 230 235

EQUUS - Unstructured

<210> 81
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..26

<220>
 <221> CDS
 <222> 27..689

<220>
 <221> 3'UTR
 <222> 690..1406

<220>
 <221> polyA_signal
 <222> 1302..1307

<220>
 <221> polyA_site
 <222> 1325..1406

<400> 81
 cccggaaatgc cgcaagg atg gcg gga ggg gtg cgc ccg ctg cgg 53
 Met Ala Gly Gly Val Arg Pro Leu Arg
 -30 -25
 ggc ctc cgc gcc ttg tgt cgc gtg ctg ctc ttc ctt tcg cag ttc tgc
 Gly Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys 101
 -20 -15 -10
 att ctg tcg ggc ggt gaa agt act gaa atc cca cct tat gtg atg aag
 Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys 149
 -5 1 5 10
 tgt ccg agc aat ggt ttg tgt agc agg ctt cct gca gac tgt ata gac
 Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp 197
 15 20 25
 tgc aca aca aat ttc tcc tgt acc tat ggg aag cct gtc act ttt gac
 Cys Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp 245

卷之三

35	40	45
Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn		
50	55	60
Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys		
65	70	75
Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr		
85	90	95
Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg		
100	105	110
Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp		
115	120	125
Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp		
130	135	140
Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser		
145	150	155
Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly		
165	170	175
Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile		
180	185	

TDS000 - Drosophila

<210> 83
<211> 1754
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..510

<220>
<221> 3'UTR
<222> 511..1754

<220>
<221> polyA_signal
<222> 1718..1723

<220>
<221> polyA_site
<222> 1739..1754

<400> 83	60	
tcccccggccg ccgcgggtgc gtcgcggcg ctgcactga agccccggcc ctgcgcgc		
gggttgcgc cccgacgctc gccccctgc accccggcg gccgttagggc ggtaacg	117	
atg ctg cgg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc	165	
Met Leu Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu		
-20	-15	-10
ctg tgc ccc ggg cac gtc ggc gga ctg tgg ggt gtg ggc agc ccc	213	
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro		
-5	1	5
ttg gtt atg gac ccc acc agc atc tgc agg aag gca cgg cgg ctg gcc	261	
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala		
10	15	20
25		
ggg cgg cag gcc gag ttg tgc cag gct gag cgg cga gaa gtg gtg gca gag	309	
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu		
30	35	40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc	357	
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe		
45	50	55

cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100 105
 ggc ccc agc tgaccgcccc agcccgctg gattgcacct gtctgcattc 550
 Gly Pro Ser
 acagacattt gggagacggc cttctgttcc gccatcaactg cggccggcgc cagccacggc 610
 gtcaacggcagg ctgttctat gggcgagctg ctgcgtggc gtgcggcaggc gcccggcggg 670
 cggggcccttc cggggcccttc cgggtcgccc ggcacccccc gacccctgg ccccgccggc 730
 tcccccggaaag gggcgcccg ctggggagtgg gggaggctggc ggcacgcgtt ggacttcggg 790
 gacggaaatg cggaggcttt tgcgtacggc cggcacaacg ggggacggcgg agacateccgc 850
 gcgttggtgtc aactgtcaca aaacaggaggc ggcaggctgg cctgtcgagg ccacacgcgc 910
 acccgagtgc aatgcacccgg gctgtcgaaa tcatgcgcgc tgccgacccctg ctggcagaag 970
 ctgcattccat ttgcggggat gggcgccggc ctgttgaggc gcttccacgg cgccctcacgc 1030
 gtcatggca ccaacgcggc caaggccctt ctggccggcc tccgcacgcgtt caagccgcgc 1090
 ggccgagccg accctctcta cggccgcgtat tccgcgcact tctggccccc caacccgacgc 1150
 acggcgccccc cggcgcacggc cggtecgccgc tgcaatagca ggcggccggc cctcagccgc 1210
 tgccgacctgc tggtgtcgcc cggccggcgc cggcaggaga gctgtcgactt cgaagagaac 1270
 tgctctgtcc gtttccactgc gtgtcgctta gtacagtgc acccgctggc tggtcgcaag 1330
 gagctcgcggc ttgcgtgtc accccgcgcgc cggccgcgtt actgtacttc egcagcgggt 1390
 gtcgcacccctt gtgggacccgc agggcaccggc caccggggcgc ctctgcgcgc tcgagcccg 1450
 ctctccctgc ccaaaccggc accccgggctt ctgtggaaat ggttggggca ggggcttgag 1510
 aggaacccccc accggcggaa gcccggggc ccagacggcc cccaaaaaggc gctcggggag 1570
 cgttaaagg acactgtaca ggccttcctt cccttggcc tctaggagga aacagttttt 1630
 taactgtggaa aaaaggccatg ctaaaggctt ctggatactg ggttcccccag aactgtgtgc 1690
 cacaggatgg tgggtggatg tagtatcaat aaagatattt aaccaccaa aaaaaaaaaaa 1750
 aaaaa 1754

<210> 84
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 84
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 Leu Cys Pro Ala His Val Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 25 30 35 40
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 Arg Phe Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100
 Gly Pro Ser
 105

<210> 85

<211> 1754
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..510

<220>
<221> 3'UTR
<222> 511..1754

<220>
<221> polyA_signal
<222> 1718..1723

<220>
<221> polyA_site
<222> 1739..1754

<400> 85
tccccggccg cggccgttgc gtcgcccgcg ctgcactga agccggggcc ctgcgcgc
cggtttcgcc cccgacgcctc gccccctgcc caccggggcg gccgttagggc ggtaacg 60
atg ctg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccc gag ctc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gtc gat gag ccg gaa gtt gtt gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct cgg ggc gcc cgg ctc ggg gtc cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Gly Cys Gln Phe Gln Phe
45 50 55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
75 80 85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90 95 100 105
ggc ccc agc tgaccgcccc agccgcgtt gattgcacct gtctgcattc 550
Gly Pro Ser
acagacattc gggagaacggc ctgcgtgttc gecatcaactg cggccggcg cagccacgc 610
gtcacggcagg ctgttttat gggcgacgtg ctgcagtgcg gtcggccagg gccccgggg 670
cgggcccttc cccggcccttc cggcctgccc ggcacccccc gaccccccggg ccccccgggg 730
tccccggggc gcaacggccgc ctggggatggggatggggatggggatggggatggggatgggg 790
gacggaaatg cgaggctttt tatggacggc cggccacaage gggggacggg agacatccgc 850
gcgttgttgc aactgcacaa caacggacggc ggcaaggctgg cctgtggggag cacaacgcgc 910
accggatgc aatggccacgg gctgtggggatggggatggggatggggatggggatggggatgggg 970
ctggcttcat ttccgcggatgg gggcgccggg ctgtggggatggggatggggatggggatggggatgggg 1030
gtcatggcca ccaacgcacgg caaggccctg ctggccggcc tcggcacgtt caagccggcc 1090
ggccgacggc acctccctcta cggccgcgtt tgcggccccc caacccgcgc 1150

accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgcggga cctcagccgc 1210
tgcgacactgc tgtgtcgcc cccggggcac cgcggaggaga gctgtcagct cgaagagaac 1270
tgccctgtgcc gcttccactg gtgtcgta gtacagtgc accgtgtcc cgtagtgc 1330
gaggtcgcc gtcgcctgtg accccggcc cggcgctag actgacttcg cgcacgggtg 1390
gtctcgacactt gtgggaccc tcggcggcc agggcaccgg cacccggggc ctctcgccg ttagggcc 1450
cctctccctg cccaaagccca actccccagg ctctggaaat gttggggcgaa gggggctttag 1510
aggaacgccc accccacgaag gcccgaggcg ccacacggcc cccggaaaggc gctcggggag 1570
cgttttaaagg acactgtaca ggccctccct ccccttggcc tctaggagga aacagtttt 1630
tagactggaa aaaagccagt ctaaaaggct ctggatactg gggtccccag aactgtgtgc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatattt aaaccaccaa aaaaaaaaaa 1750
aaaaa 1754

<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..24

<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25 30 35 40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
75 80 85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90 95 100
Gly Pro Ser
105

<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..151

<220>
<221> CDS
<222> 152..655

<220>
<221> 3'UTR
<222> 656..1431

<220>
<221> polyA_signal
<222> 1399..1404

<220>

<221> polyA_site
<222> 1416..1431

<400> 87
aattttttctt cacaaggact gggtaagag ttctgcagcc ttacagagac tggaaaagaa 60
gccccaaacc a gggcccccag agaggctccc caggccccctt tggttcctcg agcctcagct 120
ggagatccgg cgccaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
Met Leu Phe Arg Leu Ser Glu
1 5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Pro Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
10 15 20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
25 30 35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
40 45 50 55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Ala Ser Glu Glu Glu Asp Glu
60 65 70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
75 80 85
gaa gag gag gat gaa gaa gag gaa gaa gag gac agc cag gtc 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
90 95 100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
105 110 115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Leu Asp Glu
120 125 130 135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
140 145 150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
155 160 165
aca taggcaccca gcctgcatc cccaggagga agtgtgggg acatcgctgt 705
Thr
tccccggaaaa cccactctat cctcacccctg ttttgtgctc ttccccctgc ctgcttagggc 765
tgccggttctt gacttctaga agactaaggc tggtctgtgt ttgtctgttt gcccacccctt 825
ggctgataacc cacaaggactt gggcaactc tgccctgtgc tgcctgtatc ccaacccctgc 885
tccatttcacc cagcggggagg tgggtatgtgaa gacagcccc attgaaaaat ccggaaaaacc 945
ggggaaacgggg atttgcctt cacaatccctt ccccccggat ccttcccccgtt ggacacacgg 1005
gaccacccagg ggaggacccctt aagatctggg gaaaggagggt ctgtggaaacc ttggggatcc 1065
cttagatccct ttcttaccca ctttccatag gaggattcca agtccacccat tcttcacccg 1125
gtttcttaccca gggccaggaga ctaaggccgtt ttcttcataa gcttcaacat ttggggaaatc 1185
ttcccttaata cacccttgcgtt cctccctgggt gcttggaaaga tgactggca gagaccttt 1245
tgttgtcggtt ttgtgtttttt gtcaggaaat gcccggatgtt ttatgttccccggggggcact 1305
acacgggggg ggcggagggtt ttctttgtcc cccaggctgtt ctggccctttt ccccttcttc 1365
cctgactccca ggcctgaacc cttccctgtc tgtaataaat ttggtaaag aaaaaaaaaa 1425
aaaaaaa 1431

<210> 88
<211> 168
<212> PRT
<213> Homo sapiens

<400> 88
Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1 5 10 15

Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
 20 25 30
 Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
 35 40 45
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
 50 55 60
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
 65 70 75 80
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
 85 90 95
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
 100 105 110
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
 115 120 125
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
 130 135 140
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
 145 150 155 160
 Pro Ser Pro Ser Glu Pro Gly Thr
 165

YJGEGD

<210> 89
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

<400> 89
 attttttct cacaaggact gggtaagag ttctgcagcc ttacagagac tgaaaaagaa 60
 gccccaaacca agggcccccag agaggcccc caggccccctt tgggtccctg agcctcagct 120
 ggatcccg cgccaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
 Met Leu Phe Arg Leu Ser Glu
 1 5
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
 His Ser Ser Pro Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
 10 15 20
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
 Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
 25 30 35
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
 40 45 50 55
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Asp Glu

60	65	70		
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag			412	
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Asp Glu Glu				
75	80	85		
gaa gag gag gat gat gaa gag gaa gaa gag gac agc cag gct			460	
Glu Glu Asp Asp Glu Glu Glu Glu Glu Asp Ser Gln Ala				
90	95	100		
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt			508	
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys				
105	110	115		
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc ect ctg gat gag			556	
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Leu Asp Glu				
120	125	130	135	
tcc gag aga gat gga ggc ttc gag gac caa gtg gaa gac cca goa cta			604	
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu				
140	145	150		
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc			652	
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly				
155	160	165		
aca taggcaccca gcctgcata cccaggagga agtggagggg acatcgctgt			705	
Thr				
tccccggaaa cccactctat cctcacccctg ttttgtgctc ttcccctgc ctgcttagggc			765	
tgccggcttc gacttctaga agactaaggc tggtctgtgt ttgttgttt gcaccacattt			825	
ggctgtatacc cagagaacctt gggcaacttc tgccgtatgc ccacccctgc cagtcatcc			885	
ggccattcacc cagcggggagg tggatgtga gacagccccat attggaaaat ccagaaaaacc			945	
ggggAACAGGGG atttgcctt cacaattcta cttcccccagat cttcccccctt ggacacaggg			1005	
ggccacacagg ggccaggacccctt aagatctggg gaaaggaggt ctggagaaacc ttgaggtaacc			1065	
cttagatccct tttagtaccca ctttccatag gaggattcca agtcaccaact ttcttcacccg			1125	
gcttctatcc ggggtccagga ctaaggcggtt ttctccata gcctcaacat ttggaaatctt			1185	
ttcccttaat cacccctgtt cctcttggtt gcctggaga tgactggca gagacctttt			1245	
tgttgctgtt tggctttga tgccaggaaat gcgcctgtat ttatgtcccc ggtggggcac			1305	
acacgcgggg ggcgcaggatt ttctttgtcc cccagctgtt ctggccctttt ccccttcttc			1365	
cctgacttcca ggctgttaacc cttccctgtc tgataataat ctttgtaaag aaaaaaaaaa			1425	
aaaaaaa			1431	

<210> 90
<211> 168
<212> PRT
<213> Homo sapiens

<400> 90			
Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser			
1	5	10	15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg			
20	25	30	
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg			
35	40	45	
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln			
50	55	60	
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr			
65	70	75	80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu			
85	90	95	
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser			
100	105	110	
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu			
115	120	125	
Arg Pro Pro Pro Leu Asp Glu Ser Gln Arg Asp Gly Gly Ser Glu Asp			
130	135	140	
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg			
145	150	155	160
Pro Ser Pro Ser Glu Pro Gly Thr			
165			

<210> 91
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..47

<220>
 <221> CDS
 <222> 48..1301

<220>
 <221> 3'UTR
 <222> 1302..1417

<220>
 <221> polyA_signal
 <222> 1360..1365

<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91
 ctccctcagttcaggccatccactggacctgggacagtgtatcgacataatgcgttct
 Met Pro Ser
 tctgtcttcgttgtggatctctctgtgtatggctgtctgtgtctgtgtctgtgtct
 Ser Val Ser Trp Gly Ile Leu Leu Ala Gly Leu Cys Cys Leu Val
 -10 -5
 -20 -15 -10 -5
 cctgtccatgt
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
 1 5 10
 gatacaatccatcatgatcagcatgatccaaaccatccaaatccaaatccaaatccaa
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
 15 20 25
 200
 15 20 25
 cccaaatctgt
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
 30 35 40
 248
 30
 296
 cagtttcaaacatcaccatattttttccatccatgtatgtatgtatgtatgtatgt
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
 45 50 55 60
 45
 gcctttgcataatgtttccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 65 70 75
 344
 65
 atccatgt
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 80 85 90
 392
 80
 atccatgt
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 95 100 105
 440
 95
 agccatctcagtttccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
 Ser Gln Leu Gln Leu Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 110 115 120
 488
 110
 ctgt
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 125 130 135 140
 125
 tccaaatccatgt
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 145 150 155
 584
 145
 cagatcAACGATTACGTGAGAAGGGTACTCAAAGGAAAATTGTGAT
 632

Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
 160 165 170 680
 ttg gtc aag gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac
 Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
 175 180 185 728
 atc ttc ttt aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc
 Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
 190 195 200 776
 gag gaa gag gac ttc cac gtg gac cag gcg acc acc gtg aag gtg cct
 Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val Lys Val Pro
 205 210 215 220 824
 atg atg aag cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg
 Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Leu
 225 230 235 250
 tcc agc tgg gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc
 Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile
 240 245 250 872
 ttc ttc ctg cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc
 Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu
 255 260 265 920
 acc cac gat atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct
 Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser
 270 275 280 968
 gcc agc tta cat tta ccc aaa ctg tcc att act gga acc tat gat ctg
 Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu
 285 290 295 300 1016
 aag agc gtc ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg
 Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly
 305 310 315 1064
 gct gac ctc tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag
 Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
 320 325 330 1112
 gcc gtc cat aag gct gtg ctg acc atc gag gag aaa ggg act gaa gtc
 Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala
 335 340 345 1160
 gct ggg gcc atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag
 Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu
 350 355 360 1208
 gtc aag ttc aac aaa ccc ttt gtc ttc tta atg att gaa caa aat acc
 Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr
 365 370 375 380 1256
 aag tct ccc ctc ttc atg gga aat gtg gtg aat ccc acc caa aaa
 Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys
 385 390 395 1301
 taactgcctc tcgctccatcc acccccccccc tccatccctg gccccccc tgatgcataat 1361
 taaaagggtt tagctgtt ccctgcctgc atgtgactgc aaaaaaaaaaaaaaaa 1417

<210> 92
 <211> 418
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 92
 Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
 -20 -15 -10
 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 -5 1 5
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 10 15 20

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 25 30 35 40
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 45 50 55
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 60 65 70
 His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro
 75 80 85
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 90 95 100
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 105 110 115 120
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 125 130 135
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 140 145 150
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 155 160 165
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 170 175 180
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 185 190 195 200
 Lys Asp Thr Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val
 205 210 215
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 220 225 230
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 235 240 245
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 250 255 260
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 265 270 275 280
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 285 290 295
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 300 305 310
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 315 320 325
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 330 335 340
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 345 350 355 360
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 365 370 375
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 380 385 390
 Gln Lys

<210> 93
 <211> 1115
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..277

<220>
 <221> CDS
 <222> 278..733

<220>
 <221> 3'UTR

<222> 734..1115

```
<220>
<221> polyA_signal
<222> 1072..1077
```

<220>
<221> polyA_site
<222> 1101..1115

```

<400> 93
ctctttgtc taacagacag cagcgactt aggctggata atatgtcaaat tcttacatcg
ctctttcaat gcttagtaaga tcgatgtcg ttcttttcag ttactcttca atcgccagg
tcttgatctg ctctctaaaag aagaagtata gaagataaaat ctgtcttca atacctggaa
ggaaaaacaa aataaccatca actccgtttt gaaaaaaaaat ttccaagaac ttcatcgaa
gattttactt agatgttata cacaatggaa aaaaatc atg ccc ttt ggg ctt ctg
                                         Met His Phe Gly Leu Leu
                                         -15

```

```

tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
          -10           -5            1

```

```

aaa ctt atc cat tca ttt tgc gaa ttc aat att ttc act cga cag tgc 487
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
          25           30           35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc

```

```

Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
          40           45           50
gaa gaa ttt ata tat ggg gga tgg aat cag aat cga ttt gaa      531
ctt ctt atc ttt ttt ggc gtc gtc glu glu arg arg phe glu

```

```

Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gin Asn Arg Phe Glu
      55          60          65
agt ctg gaa gag tgc aaa aaa tag tgt aca aga gat aat gca aac agg 58:
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg

```

```

Ser Ser Glu Glu Cys 70 75 80 63
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu

```

gcaata tgaacaattt tgagacactg gaagaatgcga agaacatttg tgaagatgg 78
Ala Ile
ccggatgg tccagggttga taattatgg aaccggctca atgtctgtaa taactccctg 84
actccggat caaccaagggt tccccggctt ttgtttaaca aaaaadggaa aatgtatggt 90

<210> 94
<211> 152
<212> PRT
<213> *Homo sapiens*

<220>
<221> SIGNAL
<222> 1..19

卷之三

20 cca tgt aaa gca atc atg aaa aga ttt ttc aat att ttc act cga Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg 35 34 cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg 55 54 ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca Phe Glu Ser Leu Glu Glu Lys Lys Met Cys Thr Arg Asp Asn Ala 70 69 aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys 85 84 ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr 100 99 ttt tat aac aat cag aca aca cag tgt gaa cgt ttc aag tat ggt gga Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly 115 114 tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgc agaacatttg Cys Leu Gly Asn Gln Gln Phe 135	25 30 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135	483 50 531 627 675 723 774 834 894 954 1014 1074 1134 1194 1254 1307
--	--	---

<210> 96
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..28

<400> 96 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys -25 -20 -15 Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu -10 -5 1 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys 5 10 15 20 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys 25 30 35 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu 40 45 50 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser 55 60 65 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile 70 75 80 Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu 85 90 95 100 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn 105 110 115 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly 120 125 130 Asn Gln Gln Phe	96 -25 -10 -5 1 10 15 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130	
--	--	--

<210> 97
<211> 1855
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..504

<220>
<221> 3'UTR
<222> 505..1855

<220>
<221> polyA_signal
<222> 1819..1824

<220>
<221> polyA_site
<222> 1840..1855

<400> 97
tccccggccg cggccgttgc gctcgccgctg ctgcactga agccggggcc ctgcggcgcc 60
ggcgttcggcc cggcggccccc gcggccggcg ggcgtaggcc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccg ggc cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag cgg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gtc cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
cgg ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgg ggg gag ggg gcg gaa gtg ggg ctg ctt 453
Ile Leu Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
tct ccc tgc tgt egg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100 105
gcc tgagccccac ttccccctca catgtgtctg ggccacctcg aaggaccctg 554
Ala
cctccccaggc cccctggggca gcccctcccgcc cgccagggttcc aggtccccagg ccccgactgta 614
ccggcccccaggc cccgcgtgtat tgacccgttc tgcatatccaca gacattccgg agacggccctt 674
cggtttccggc atcaactgcggg cccggccggcc acggccgttc acggccgtt gtcttatggg 734
cgagctgtcg cagtgcgggt gccaggccggcc cccggggccgg gcccctccccc gggccctccgg 794
cctggcccccggc accccccggac ccctctggccc cccggggccctc cccggaaaggca ggcggccctg 854
ggagtggggaa ggctgcggcg acgacgttgg a cttccggggac gagaaggctga ggctctttat 914
ggacgcgcggg cacaaggcgaa gacgcggaga catccgcggc ttggtgcaac tgccacaacaa 974

```

cgaggcgggc aggctggccg tgccgggcc caegcgcacc gaggtaaat gccacgggt 1034
gtcgggatcc tgcggcgctg gcacctgtgtg gcaagaatgtc ctcccttcgtt ggagggttgg 1034
cgcgccggctg ctggagggct tccacggccg tcacggccgt atgggcacca aecaggccaa 1154
ggccctgtgtg ccccgccgtcc gacgctcaa gcegcggccg cgagcgacc ttcttcacgc 1214
cgccgatccccc cccggactttt gggcccccac ccacgcacc ggtccccccg gacgcggccg 1214
tcggcgctgtg aataagcagcg cccggggactt cagcgccgtc gacgttgcgtt gtcggccggc 1334
cgggcacccgc caggagagcg tgcaagtcga agagaactgc ctgtggccgt tccacttggt 1394
ctcgcgtagta cagtggccacc gtgcggctgtg ggcgaaggag ctccagcttc ttgggtggacc 1454
cgccggccccc cccgttagact gatccggccgc acgggttgtt ccggacttgc ttggactccg 1514
gcacccggcac cggggccctc tgccggctcg agcccgacgtt ctccctgcac aagccaaact 1574
cccgaggcttc tgaaaatgtt gaggccgggg gtttggaggg acgcggccacc cacaaggccg 1634
caggggccca gacggccccc aaaggccgtt cggggccgtt taaaaggacca cttagacccgg 1694
cctccctccc ctggccctt aggaggaaac agtttttagt actggaaaaa agccaggctca 1754
aaggccgttc gatactggcc tccccggacat tgctggccac aggtgggttgg tgtaggtttag 1814
tatcaataaa gatattttaa cccaaaaaaa aaaaaaaaaa a 1855

```

<210> 98
<211> 129
<212> PRT
<213> *Homo sapiens*

<220>
<221> SIGNAL
<222> 1..24

```

<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
      -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5           1            5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60          65          70
Ile Leu Gln Gln Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
      75          80          85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
      90          95          100

```

Ala
105

<210> 99
<211> 667
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5'UTR
<222> 1..94

<220>
<221> CDS
<222> 95..613

<220>
<221> 3'UTR
<222> 614..667

<220>

<221> polyA_signal
<222> 636..641

<220>
<221> polyA_site
<222> 652..667

<400> 99
ctctgc当地 ccaggacaca cattgtgctc cgcgctccac taaaggcttg agtgggact 60
gttccatctc aacagccccct gtttgaaaa ggc atg att gtc aag ggg gtg gcc 115
Met Ile Val Lys Gly Val Ala
1 5
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
10 15 20
tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Val
25 30 35
gcc atg cct gtg ttt agg aag cag aac gaa acc aga tgg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Glu Asn Glu Thr Arg Ser Lys Gly Ile
40 45 50 55
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
60 65 70
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
75 80 85
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Tyr
90 95 100
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
105 110 115
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
120 125 130 135
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
140 145 150
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Asn Leu Lys
155 160 165
caa acc act gtg aaa aat tagctttgaa agcttatatct ggaataaaa 643
Gln Thr Thr Val Lys Asn
170
tctttcgca aaaaaaaaaaaa aaaa 667

<210> 100
<211> 173
<212> PRT
<213> Homo sapiens

<400> 100
Met Ile Val Lys Gly Val Ala Ser Arg Thr Val Val Ser Arg Pro Phe
1 5 10 15
Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
20 25 30
Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
35 40 45
Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val
50 55 60
Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
65 70 75 80

His	Gly	Tyr	Ala	Phe	Ala	Ile	Thr	Asn	Asn	Gly	Tyr	Ile	Leu	Thr	His
						85					90				95
Pro	Glu	Leu	Arg	Leu	Leu	Tyr	Glu	Glu	Gly	Lys	Lys	Arg	Arg	Lys	Pro
						100				105					110
Asn	Tyr	Ser	Ser	Val	Asp	Leu	Ser	Glu	Val	Glu	Trp	Glu	Asp	Arg	Asp
						115				120					125
Asp	Val	Leu	Arg	Asn	Ala	Met	Val	Asn	Arg	Lys	Thr	Gly	Lys	Phe	Ser
						130				135					140
Met	Glu	Val	Lys	Lys	Thr	Val	Asp	Lys	Gly	Val	His	Phe	Ser	Gln	Thr
						145				150					160
Phe	Leu	Leu	Leu	Asn	Leu	Lys	Gln	Thr	Thr	Val	Lys	Asn			
						165				170					

<210> 101
<211> 1062
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5'UTR
<222> 1..153

<220>
<221> CDS
<222> 154..639

<220>
<221> 3'UTR

<220>
<221> polyA_signal
<222> 1023 1028

<220>
<221> polyA_site
<222> 1047..1062

```

<400> 101
atttgtatggcttgcg caataactga tggctgttc ccctcctgt ttatcttca
gttaatgacc agccacggcg tcctctgt gactctggc egctgcctt cagggtccc
gagccacacg ctgggggtgc tggctgaggg aac atg ctg tgt tgg ctg cag ctg
Met Ala Cys Trp Pro Gln Leu
1 5
agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aca aca tgc 222
Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Gln Thr Cys
10 15 20
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
25 30 35
atc tct gtt cgg ctg agc tac cca ccc tat gaa cca cat gaa tgc cat 318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
40 45 50 55
ttt cca aat aaa gcc atg ccc ttt gca gga aca ctt cct tgg gtt cag 366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
60 65 70
ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
75 80 85
ggg gag gct ccc gga gtt gga aac ttt aac aaa tcc att gtg gct 462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
90 95 100
cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510

```

Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp
 105 110 115
 acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc 558
 Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
 120 125 130 135
 aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag 606
 Lys Lys Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
 140 145 150
 aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtctt cattgtcagg 659
 Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
 155 160
 cctctaagcc caagccaagc catcgcatcc ccttgactt gcacatatac gcccagatgg 719
 cctgaagtaa ctgaagaatc acaaagaatg tgaaaaggcc ctgcctcgcc ttaactgtatg 779
 acgttccacc attgtgattt gtctctgccc caccctaaatc gatgtatcaa ccctgtgaat 839
 ttcccttccc tggttcagaa gctccccccac tgacccctt tgacccctt gcccctgccc 899
 accagagaaac aacccttttctt gatgtatcaa ttccattacc ttcccaaatc ctataaaacg 959
 gccccccccc tatctccctt tgctgactt cttttcgac tcagccccc tgcaagccagg 1019
 tggaaaaaaaac agctttattt ctcacacaaaa aaaaaaaaaaaa aaa 1062

<210> 102
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Trp Lys Asn Leu Thr
 1 5 10 15
 Phe Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
 20 25 30
 Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
 35 40 45
 Tyr Glu Gln His Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
 50 55 60
 Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
 65 70 75 80
 Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
 85 90 95
 Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
 100 105 110
 Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
 115 120 125
 Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
 130 135 140
 Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
 145 150 155 160
 Leu Leu

<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..149

 <220>
 <221> CDS
 <222> 150..392

 <220>
 <221> 3'UTR
 <222> 393..933

<220>
<221> polyA_site
<222> 63..933

<400> 103
aaaccctcag ggacctggta tagacgcaga atctgtttca cacaacaact gctatttcaa 60
ggaaaaaaaaaaa aaaaagaacg aaatgatacc aagacaacgt cataaacagag atccaatcg 120
cagatgtga cgatgaaaa tacagttag atg agt cag aaa ccg gcc aag gag 173
Met Ser Gln Lys Pro Ala Lys Glu
1 5
ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
10 15 20
cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
25 30 35 40
gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
45 50 55
gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
Glu Glu Asp Pro Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
60 65 70
aag atc agg cca acc cca aag aag aag tgaccaagg ggagttaaa 412
Lys Ile Arg Pro Thr Pro Lys Lys Lys
75 80
ytgatgtaa aacctccggct ctgtggactca ttgtttcacc acccatctac ccctggatga 472
agttatctgg cttaaatat tatgcagggg caaacacccgt ctgtatgtgc aactgtgtat 532
gtctatggc cccatggcat gggggcctca gggcagcctg ctgtggatgtc tttaaagatg 592
tcatccccat gtcttctgac ctctataat gcacactgaga gatctgtgtc cagttctgtc 652
atctcccac gggactcaagt ttcttcataat tgaatagatata ttgtttcttc caaggacatg 712
tggaaaaaaaaaaa aaagatgtta tacaaccatc aaatggccaa aaataaaaaaa aattggctgg 772
ggctgtgtggc gggcgcctgt ggccccatgt ctgtggagg ctgaggcagg agaatggcgt 832
gaaacctggga ggcggagctt gcagtgagcc gagatcgcac cactgtcactc cagcctggc 892
gacagagcga gactctgtct caaacaaaaaa aaaaaaaaaa a 933

<210> 104
<211> 81
<212> PRT
<213> Homo sapiens

<400> 104
Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
1 5 10 15
Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
20 25 30
Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
35 40 45
Ser Gly Cys Phe Tyr Gln Lys Lys Glu Asp Trp Ile Cys Cys Ala
50 55 60
Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
65 70 75 80
Lys

<210> 105
<211> 1187
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..34

<220>
<221> CDS
<222> 35..1069

<220>
<221> 3'UTR
<222> 1070..1187

<220>
<221> polyA_signal
<222> 1146..1151

<220>
<221> polyA_site
<222> 1172..1187

<400> 105
accacattttgg tagtgccagt gtgactcata caca atg att tct cca gtc ctc atc 55
Met Ile Ser Pro Val Leu Ile
-15
ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103
Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys
-10 -5 1 5
ccc aag cca gat gat tta cca ttt tcc aca gtc gtc ccg tta aaa aca 151
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr
10 15 20
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr
25 30 35
gtg ctc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247
Val Ser Arg Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu
40 45 50
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala
55 60 65
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Phe Glu Tyr Pro
70 75 80 85
aac acg atc aca ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala
90 95 100
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro
105 110 115
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca 487
Val Cys Ala Pro Ile Ile Cys Pro Pro Ser Ile Pro Thr Phe Ala
120 125 130
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg
135 140 145
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat 583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn
150 155 160 165
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa 631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu
170 175 180
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt 679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe
185 190 195
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gca aca 727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr
200 205 210
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa 775

<210> 106
<211> 345
<212> PRT
<213> *Homo sapiens*

<220>
<221> SIGNAL
<222> 1..19

Tyr	Tyr	Lys	Asp	Lys	Ala	Thr	Phe	Gly	Cys	His	Asp	Gly	Tyr	Ser	Leu
				210				215					220		
Asp	Gly	Pro	Glu	Glu	Ile	Glu	Cys	Thr	Lys	Leu	Gly	Asn	Trp	Ser	Ala
							225		230				235		
Met	Pro	Ser	Cys	Lys	Ala	Ser	Cys	Lys	Val	Pro	Val	Lys	Lys	Ala	Thr
							240		245			250			
Val	Val	Tyr	Gln	Gly	Glu	Arg	Val	Lys	Ile	Gln	Glu	Lys	Phe	Lys	Asn
							255		260			265			
Gly	Met	Leu	His	Gly	Asp	Lys	Val	Ser	Phe	Phe	Cys	Lys	Asn	Lys	Glu
							270		275		280				285
Lys	Lys	Cys	Ser	Tyr	Thr	Glu	Asp	Ala	Gln	Cys	Ile	Asp	Gly	Thr	Ile
							290		295				300		
Glu	Val	Pro	Lys	Cys	Phe	Lys	Glu	His	Ser	Ser	Leu	Ala	Phe	Trp	Lys
							305		310			315			
Thr	Asp	Ala	Ser	Asp	Val	Lys	Pro	Cys							
							320		325						

<210> 107
<211> 1520
<212> DNA
<213> *Homo sapiens*

<220>
<221> 5'UTR
<222> 1..15

<220>
<221> CDS
<222> 16..1449

<220>
<221> 3' UTR
<222> 1450..1520

<220>
<221> polyA_signal
<222> 1483..1488

<220>
<221> polyA_site
<222> 1505..1520

```

<400> 107
ttttttttg acaag atg gcg gca gga ggc agt ggc gtt ggt ggg aag cgc 51
      Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg
      1           5           10
agc tcg aaa agc gat gcc gat tct ggt ttc ctg ggg ctg cgg ccc act 99
Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr
      15          20          25
tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag 147
Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys
      30          35          40
aag cgg ggc tgg cgg cgg ctt gct cag gag cgg ctc ggg ctg gag gtt 195
Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val
      45          50          55          60
gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc 243
Asp Gln Phe Leu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly
      65          70          75
ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc 291
Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe The Val Asp Thr Gly
      80          85          90
tcc aag gaa aaa ggg ctg aca aag aag aca acc aaa gtc cag aag aag 339
Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys

```

	95	100	105	
tca ctg ctt ctc aag aaa ccc ctt cgg gtt gac ctc atc ctc gag aac				387
Ser Leu Leu Leu Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn				
110	115	120		
aca tcc aaa gtc ctc gcc ccc aaa gac gtc ctc gcc cac cag gtc ccc				435
Thr Ser Lys Val Pro Ala Pro Lys Asp Val Ala His Gln Val Pro				
125	130	135	140	
aac gcc aag aag ctc agg cgg aag gag cag cta tgg gag aag ctg gcc				483
Asn Ala Lys Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala				
145	150	155		
aag cag ggc gag ctg ccc cgg gag gtc cgc agg gcc cag gcc cgg ctc				531
Lys Gln Gly Glu Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu				
160	165	170		
ctc aac cct tct gca aca agg gcc aag ccc ggg ccc cag gag acc gta				579
Leu Asn Pro Ser Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val				
175	180	185		
gag cgg ccc ttc tac gag ctc tgg gcc tca gac aac ccc ctg gag agg				627
Glu Arg Pro Phe Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg				
190	195	200		
ccg ttg gtt ggc cag gag ttt ttc ctg gag cag acc aag aag aag aaa				675
Pro Leu Val Gly Gln Asp Glu Phe Leu Glu Gln Thr Lys Lys Lys				
205	210	215	220	
gga gtg aag cgg cca gca cgc ctg cac acc aag ccg tcc cag gca ccc				723
Gly Val Lys Arg Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro				
225	230	235		
gcc gtg gag gtc gcg cct gcc gga gct tcc tac aat cca tcc ttt gaa				771
Ala Val Glu Val Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu				
240	245	250		
gac cac cag acc ctg ctc tca gcg gcc cac gag gtg gag ttg cag cgg				819
Aep His Gln Thr Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg				
255	260	265		
cag aag gag gcg gag aag ctg gag cgg cag ctg gcc ctg ccc gcc acg				867
Gln Lys Glu Ala Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr				
270	275	280		
gag cag gcc acc cag gag tcc aca ttc cag gag ctg tgc gag ggg				915
Glu Gln Ala Ala Thr Glu Ser Thr Phe Glu Leu Cys Glu Gly				
285	290	295	300	
ctg ctg gag gag tcg cat ggt gag ggg gag cca ggc cag ggc gag ggg				963
Leu Leu Glu Glu Ser Asp Gly Glu Pro Gly Gln Gly Glu Gly				
305	310	315		
ccg gag gct ggg gat gcc gag gtc tgt ccc acg ccc gcc cgc ctg gcc				1011
Pro Glu Ala Gly Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala				
320	325	330		
acc aca gag aag acg gag cag cag cgg cgg cgg gag aag gct gtg				1059
Thr Thr Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val				
335	340	345		
cac agg ctg cgg gta cag cag gcc ggc ttg cgg gcc gcc cgg ctc cgg				1107
His Arg Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg				
350	355	360		
cac cag gag ctg ttc cgg ctg cgc ggg atc aag gcc cag gtg gcc ctg				1155
His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu				
365	370	375	380	
agg ctg gcg gag ctg gcg cgg cgg cag agg cgg cgg cag gcg cgg cgg				1203
Arg Leu Ala Glu Leu Ala Arg Arg Gln Arg Arg Gln Ala Arg Arg				
385	390	395		
gag gct gag gct gac aag ccc cga agg ctg ggg cgg ctc aag tac cag				1251
Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln				
400	405	410		
gca cct gac atc gac gtg cag ctg agc tgc gag ctg aca gac tcc ctc				1299
Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu				
415	420	425		
agg acc ctg aag ccc gag ggc aac atc ctt cga gac cgg ttc aag agc				1347
Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser				

430	435	440	
ttc cag agg aat atg atc gag cct cga gag aga gcc aag ttc aaa			1395
Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys			
445	450	455	460
cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc			1443
Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile			
465	470	475	
cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaa aatctttctt			1499
Gln Leu			
agctcaaaaa aaaaaaaaaa a			1520

<210> 108
<211> 478
<212> PRT
<213> Homo sapiens

<400> 108			
Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser			
1	5	10	15
Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro			
20	25	30	
Ala Leu Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp			
35	40	45	
Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu			
50	55	60	
Glut Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu			
65	70	75	80
Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys			
85	90	95	
Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu			
100	105	110	
Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val			
115	120	125	
Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys			
130	135	140	
Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu			
145	150	155	160
Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser			
165	170	175	
Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe			
180	185	190	
Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly			
195	200	205	
Gln Asp Glu Phe Leu Glu Gln Thr Lys Lys Gly Val Lys Arg			
210	215	220	
Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val			
225	230	235	240
Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr			
245	250	255	
Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala			
260	265	270	
Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala			
275	280	285	
Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu			
290	295	300	
Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly			
305	310	315	320
Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys			
325	330	335	
Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg			
340	345	350	
Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu			
355	360	365	

Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu
 370 375 380
 Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala
 385 390 395 400
 Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile
 405 410 415
 Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys
 420 425 430
 Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg
 435 440 445
 Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys
 450 455 460
 Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
 465 470 475

<210> 109
 <211> 1789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..94

<220>
 <221> CDS
 <222> 95..1252

<220>
 <221> 3'UTR
 <222> 1253..1789

<220>
 <221> polyA_signal
 <222> 1751..1756

<220>
 <221> polyA_site
 <222> 1774..1789

<400> 109
 ggttttgcattttttttctt gttttcggtt agatgggagg cccggggacc tggctgggtt 60
 ttcggcaagg ttctccgata cccaggtttc ataa atg tgg ttg ctt tcc tgc 115
 Met Cys Leu Leu Ser Cys
 -10

cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163
 Pro Cys His Pro Ser Ala His Gln Ser Met Trp Ile Glu Arg Thr
 -5 1 5

tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211
 Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu
 10 15 20 25

gtg gtg cac atg tcg cag acc aca att agt cct ctg gag aat gcc ata 259
 Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile
 30 35 40

gaa acc atg tcc acg gcc aat gag aag atc ctg atg atc aac cag 307
 Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln
 45 50 55

tac cag agt gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg 355
 Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu
 60 65 70

aac ggg att gtg gac cct gct gtc atg gga ggc ttc gcc aag tat gag 403
 Asn Gly Ile Val Asp Pro Ala Val Met Gly Phe Ala Lys Tyr Glu
 75 80 85

aag gcc ttc act gaa gag tat gtc agg gac cac cct gag gag cag	451
Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg Asp His Pro Glu Asp Gln	
90 95 100 105	
gac aag ctg acc cac ctc aag gac ctg att gca tgg cag atc ccc ttc	499
Asp Lys Ieu Thr His Leu Lys Asp Leu Ile Ala Trp Gln Ile Pro Phe	
110 115 120	
ttg gga gct ggg att aag atc cat gag aaa agg gtg tca gat gag aac ttg	547
Leu Gly Ala Gly Ile Lys Ile His Lys Arg Val Ser Asp Asn Leu	
125 130 135	
cga ccc ttc cat gag cgg atg gag gaa tgt ttc aag aac ctg aaa atg	595
Arg Pro Phe His Asp Arg Met Glu Glu Cys Phe Lys Asn Leu Lys Met	
140 145 150	
aag gtg gag aag gag tac ggt gtc cga gag atg cct gag ttt gag gac	643
Lys Val Glu Lys Glu Tyr Gly Val Arg Glu Met Pro Asp Phe Asp Asp	
155 160 165	
agg aag gtg ggc cgt ccc agg tct atg ctg cgc tca tac aga cag atg	691
Arg Arg Val Gly Arg Pro Arg Ser Met Leu Arg Ser Tyr Arg Gln Met	
170 175 180 185	
tcc atc atc ttg ctg gct tcc atg aat tct gag tgc agc acc ccc agc	739
Ser Ile Ile Ser Leu Ala Ser Met Asn Ser Asp Cys Ser Thr Pro Ser	
190 195 200	
aag cct acc tca gag agg ttt gac ctg gaa tta gca tca ccc aag acg	787
Lys Pro Thr Ser Glu Ser Phe Asp Leu Glu Leu Ala Ser Pro Lys Thr	
205 210 215	
ccg aga gtg gag gag gaa ccg atc tcc ccg ggg agc acc ctg cct	835
Pro Arg Val Glu Gln Glu Glu Pro Ile Ser Pro Gly Ser Thr Leu Pro	
220 225 230	
gag gtc aag ctg cgg agg tcc aag aag agg aca aag aga agc agc gta	883
Glu Val Lys Leu Arg Arg Ser Lys Lys Arg Thr Lys Arg Ser Ser Val	
235 240 245	
gtt ttt ggc gat gag aaa gca gct gca gag tcg gac ctg aag cgg ctt	931
Val Phe Ala Asp Glu Lys Ala Ala Ala Glu Ser Asp Leu Lys Arg Leu	
250 255 260 265	
tcc agg aag cat gag ttc atg agt gac acc aac ctc tcg gag cat gcg	979
Ser Arg Lys His Phe Met Ser Asp Thr Asn Leu Ser Glu His Ala	
270 275 280	
gcc atc ccc ctc aag gag cgc tct gtc ctc tct caa atg agc aac ttg	1027
Ala Ile Pro Leu Iys Ala Ser Val Leu Ser Gln Met Ser Phe Ala Ser	
285 290 295	
cag tcc atg cct acc atc cca gcc ctg gcg ctc tca gtg gca ggc atc	1075
Gln Ser Met Pro Thr Ile Pro Ala Leu Ala Leu Ser Val Ala Gly Ile	
300 305 310	
cct ggg ttg gat gag gcc aac aca tct ccc cgc ctc agc cag acc ttc	1123
Pro Gly Leu Asp Glu Ala Asn Thr Ser Pro Arg Leu Ser Gln Thr Phe	
315 320 325	
ctc caa ctc tca gat ggt gac aag aag aca ctc aca cgg aag aag gtc	1171
Leu Gln Leu Ser Asp Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val	
330 335 340 345	
aat gag ttc ttc aag aca atg ctg gcc agc aaa tcg gct gaa gaa ggc	1219
Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly	
350 355 360	
aaa gag atc cca gag tcc ctg tcc acg gag ctg tgagctgtct ctgactagg	1272
Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu	
365 370	
ctgcatggaa gagccaggaga gggggatttc tgaaaggaga aagccatcgcc tggacatcg	1332
aaggcttcaga gagtgggaga ctgtccccat cagtgttct tacttagagg agacagagag	1392
gccaatcgcc tcccaagact tggatcta caaaggccac atccccggat ctgtgtatca	1452
tggtgatca ggaagcttc acgttagattt ctgaaactcaa ggttccatcgatccatataa	1512
ctcccaatgt gctttccca acatccatcg cacatgtttt ataaaccatgt ttctttagt	1572
taaaaaatct ttttatatctt attttagattt aacatgtttt tactttatcat tttttatata	1632
aaaaaccatcg ttcttttgtt acggcaatct ctgtggatcg tgctgtttc ttactgtacaa	1692
taaaaaatctt ctgttttgtt caaaaaaaaaaaaaaaa	1752

<210> 110
<211> 386
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..15

<400> 110
Met Cys Leu Leu Leu Ser Cys Pro Cys His Pro Ser Ala His Gly Gln
-15 -10 -5 1
Ser Met Trp Ile Glu Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro
5 10 15
Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
20 25 30
Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
35 40 45
Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
50 55 60 65
Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
70 75 80
Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
85 90 95
Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
100 105 110
Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
115 120 125
Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
130 135 140 145
Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
150 155 160
Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
165 170 175
Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
180 185 190
Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
195 200 205
Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
210 215 220 225
Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
230 235 240
Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
245 250 255
Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
260 265 270
Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
275 280 285
Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
290 295 300 305
Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
310 315 320
Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
325 330 335
Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
340 345 350
Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr
355 360 365
Asp Leu
370

<210> 111

<211> 1408
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..102

<220>
<221> CDS
<222> 103..1263

<220>
<221> 3'UTR
<222> 1264..1408

<220>
<221> polyA_signal
<222> 1341..1346

<220>
<221> polyA_site
<222> 1365..1408

<400> 111
cttcttgact ctctgttcac agaactcagg ctgcctccag ccagcctttg cccgcttagac 60
tcactggccc tgatcaacttg aagggtgcgc aagtcaactga ga atg agc act ttc 114
Met Ser Thr Phe
1
ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
5 10 15 20
ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210
Gly Thr Val Phe Cys Lys Tyr Lys Ser Ser Gly Gln Leu Trp Ser
25 30 35
tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258
Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Ile Leu
40 45 50
tcc cct ttt tgg ggc ttg atc ctc ttc tgc gtg tca tgc ttc ctc atg 306
Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
55 60 65
tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
70 75 80
gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys
85 90 95 100
tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450
Tyr Leu Asp Glu Leu Gly Phe Thr Val Ala Gly Val Leu Asn Glu
105 110 115
aat ggc cca gga gct gag gaa ttg cga aca acc tgc tct ccg cgc ctc 498
Asn Gly Pro Gly Ala Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu
120 125 130
tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546
Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala
135 140 145
tat agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
150 155 160
atc aac aat gct ggg gtt ctt ggc ttc act gat ggg gag ctt ctt 642
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu
165 170 175 180
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act 690

YUSQG0 = ONEHEGO

Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr			
185	190	195	
gtg gag gtc aca aag acg ttt ttg ctt ctt aga aaa tcc aaa ggg			738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly			
200	205	210	
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtc gaa agg			786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg			
215	220	225	
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca			834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser			
230	235	240	
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc			882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile			
245	250	255	260
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg			930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp			
265	270	275	
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag			978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln			
280	285	290	
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta			1026
Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu			
295	300	305	
ttg atc aac tcg tta gcc agc aag gac ttc tct ccg gtg ctg cgg gac			1074
Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp			
310	315	320	
att cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac aeg cca			1122
Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro			
325	330	335	340
ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att			1170
Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile			
345	350	355	
ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc			1218
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro			
360	365	370	
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc			1263
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Ala Pro			
375	380	385	
taggaatgg aagccctcaa agaagtccga atgtcatagt ctggaaatga aaggaaaact	1323		
ggggaaattgg gtttctcatt aaagtgttt cccactctgt waaaaaaaaaaaaaaa	1383		
aaaaaaaaaga aaaaaaaaaaaa aaaaa	1408		

<210> 112

<211> 387

<212> PRT

<213> Homo sapiens

<400> 112			
Met Ser Thr Phe Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro			
1	5	10	15
Thr Val Leu Cys Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly			
20	25	30	
Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys			
35	40	45	
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser			
50	55	60	
Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val			
65	70	75	80
Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His			
85	90	95	
Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly			
100	105	110	
Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys			

	115	120	125	
Ser Pro Arg Leu Ser Val	Leu Gln Met Asp Ile Thr	Lys Pro Val Gln		
130	135	140		
Ile Lys Asp Ala Tyr Ser	Lys Val Ala Ala Met Leu Gln Asp Arg Gly			
145	150	155	160	
Leu Trp Ala Val Ile Asn Asn Ala Gly	Val Leu Gly Phe Pro Thr Asp			
	165	170	175	
Gly Glu Leu Leu Met Thr Asp Tyr	Lys Gln Cys Met Ala Val Asn			
	180	185	190	
Phe Phe Gly Thr Val Glu Val Thr	Lys Thr Phe Leu Pro Leu Leu Arg			
	195	200	205	
Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala				
	210	215	220	
Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr				
	225	230	235	240
Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys				
	245	250	255	
Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr				
	260	265	270	
Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro				
	275	280	285	
Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg				
	290	295	300	
Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro				
	305	310	315	320
Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala				
	325	330	335	
Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His				
	340	345	350	
Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly				
	355	360	365	
Gln Asp Lys Pro Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys				
	370	375	380	
Lys Ala Pro				
385				